


```

XX 16-ADU-1999: 9908-0471615.
XX (IDEX-) IDEX LAB INC.
XX
XX Gao H, Lawton R, Mermier B, Aiyappa AP:
XX WPI: 2001-191542/19.
XX P-PSDB: AAB72615.
XX
XX Novel canine interleukin 5 polynucleotide and polypeptides are used for
XX generating antibodies which are useful in treating allergies in dogs.
XX
XX Example 1, Fig 1: 48bp: English.
XX
XX The present invention provides the protein and coding sequences of the
XX canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
XX cancer and inflammatory reactions in dogs. The present sequence is one
XX version of the IL-5 coding sequence shown in the specification.
XX
XX Sequence 252 BP: 69 A: 54 C: 60 G: 69 T: 0 other:
XX
XX Query Match 8.7% Score 144 DB 22 Length 252
XX Best Local Similarity 100.0%: Prod. No. 70-43
XX Matches 144: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
XX
XX 27 ATGAGAAATGCTTCTGAATTTGATTTGATGCTTGGAAATGCTATGTTTGGCTTT 86
XX 1 ATGAGAAATGCTTCTGAATTTGATTTGATGCTTGGAAATGCTATGTTTGGCTTT 60
XX
XX 87 GCTGTAAAGAAATGCAATGAAATGAGTGGTGTAGAGAACTTGGAACTTGGCAATCAI 146
XX 61 GCTGTAAAGAAATGCAATGAAATGAGTGGTGTAGAGAACTTGGCAATCAI 120
XX
XX 147 CGAACTTGGCTGATAGAGGATGAG 170
XX 121 CGAACTTGGCTGATAGAGGATGAG 144
XX
XX
XX RESULT 4
XX AAZ5548
XX ID AAZ5548 standard: cDNA: 402 BP.
XX AC AAZ5548:
XX
XX 14-MAR-2000 (first entry)
XX
XX Canine interleukin-5 (IL-5) cDNA coding region.
XX
XX Interleukin-5 (IL-5) antibody: canines; inhibitor; immune response;
XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
XX Canis familiaris.
XX
XX W09961618-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999: 9960-0511942.
XX
XX 29-MAY-1998: 9608-0087306.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Jiretz MJ, Wondolting RS:
XX WPI: 2000-07262706.
XX P-PSDB: AAY58219.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 1b, Page 225: 254pp: English.

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XX
XX Sequences AAZ5549, 11-15, represent cDNA sequences
XX canine interleukin-5 (IL-5) for invention for the
XX IL-4, canine or feline IL-5, canine or
XX feline IL-5 (cDNA) and canine IL-5, canine or
XX interferon-alpha (IFN-alpha) and feline interferon-
XX colony-stimulating factor (CSF) and nucleic
XX immunoregulatory proteins, the proteins, as well as
XX nucleic acids, specific antibodies and inhibitors
XX vaccines for therapy to inhibit allergic reactions
XX response in animals (particular cats, dogs, birds,
XX they may be used to treat autoimmune or infectious
XX allergies, tumours, inflammation and graft rejection
XX the response from a co-administered antigen. The
XX can also be used for the treatment of product in
XX nucleic acid fragments are useful as probes, as well
XX as sources of inhibitory mutations (cDNA, and
XX oligonucleotides). The IL-5 may be used as a
XX screen for modulators of allergy, while the IL-5
XX detection, and in other applications.
XX
XX Sequence 402 BP: 129 A: 79 C: 60 G: 101 T: 0 other:
XX
XX Query Match 9.7% Score 144 DB 22 Length 402
XX Best Local Similarity 100.0%: Prod. No. 63-443
XX Matches 144: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
XX
XX 27 ATGAGAAATGCTTCTGAATTTGATTTGATGCTTGGAAATGCTATGTTTGGCTTT 86
XX 1 ATGAGAAATGCTTCTGAATTTGATTTGATGCTTGGAAATGCTATGTTTGGCTTT 60
XX
XX 87 GCTGTAAAGAAATGCAATGAAATGAGTGGTGTAGAGAACTTGGAACTTGGCAATCAI 146
XX 61 GCTGTAAAGAAATGCAATGAAATGAGTGGTGTAGAGAACTTGGCAATCAI 120
XX
XX 147 CGAACTTGGCTGATAGAGGATGAG 170
XX 121 CGAACTTGGCTGATAGAGGATGAG 144
XX
XX
XX RESULT 5
XX AAZ5549/c
XX ID AAZ5549 standard: cDNA: 402 BP.
XX AC AAZ5549:
XX
XX 14-MAR-2000 (first entry)
XX
XX Canine interleukin-5 (IL-5) cDNA coding region.
XX
XX Interleukin-5 (IL-5) antibody: canines; inhibitor; immune response;
XX immunoregulation; tumour; cancer; autoimmune disease; ss.
XX
XX Canis familiaris.
XX
XX W09961618-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999: 9960-0511942.
XX
XX 29-MAY-1998: 9608-0087306.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Jiretz MJ, Wondolting RS:
XX WPI: 2000-07262706.
XX P-PSDB: AAY58219.
XX
XX Nucleic acids encoding immunoregulatory proteins
XX useful for treating or preventing e.g. tumors or
XX
XX

```


allergies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used in detection, and in drug targeting.

Sequence 445 bp; 120 A; 68 C; 78 G; 79 T; 0 other;

Query Match

Best Local Similarity 100.0%; Seed No. 1186-37; Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1276 CACGACGAGCTGATTAACAGCTTTCAGGCTATAGACATTAAGACCAAGCTGC 1335
121 CACGACGAGCTGATTAACAGCTTTCAGGCTATAGACATTAAGACCAAGCTGC 180
1336 CACGACGAGCTGATTAACAGCTTTCAGGCTATAGACATTAAGACCAAGCTGC 1395
181 CACGACGAGCTGATTAACAGCTTTCAGGCTATAGACATTAAGACCAAGCTGC 240
1396 CACGACGAGCTGATTAACAGCTTTCAGGCTATAGACATTAAGACCAAGCTGC 1404
241 CACGACGAGCTGATTAACAGCTTTCAGGCTATAGACATTAAGACCAAGCTGC 249

RESULT 8

AAZ5551/c
ID AAZ5551 standard; cDNA: 445 bp.

XX AAZ5551;

14-MAR-2000 (first entry)

Canine mature Interleukin-5 (IL-5) cDNA complement.

Interleukin-5 (IL-5) antibody: canine inhibitory immune response; immunoregulation; tumour; cancer; autoimmune disease; receptor; ss.

Canis familiaris.

W09961618-AZ.

02-DEC-1999.

28-MAY-1999; 99WO-0511942.

29-MAY-1998; 98US-0087306.

(HESK-3) HESNA COKP

Shin G, Yang S, Drexler MJ, Wondolting RS;

WP1: 2000-07252/206.

P-FISH: AAV584220.

Nucleic acids encoding immunoregulatory proteins from cats or dogs, useful for treating or preventing e.g. tumors or autoimmune disease - claim 1; Page 228; 264pp; English.

Sequences AAZ5551-25551 represent cDNA sequences encoding canine Interleukin-5 (IL-5), the invention relates to canine IL-4, canine or feline IL-5 ligand, canine or feline CD40, canine or feline CD134 (CD40 ligand), canine IL-5, canine IL-13, feline Interleukin-alpha (feline IL-5), and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides which encode these immunoregulatory proteins. The proteins, their associated nucleic acids, specific antibodies and inhibitors may be used as vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans).

They may be used to treat or prevent response of Interleukin-5 allergies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used in detection, and in drug targeting.

Sequence 445 bp; 79 A; 76 C; 76 G; 79 T; 0 other;

Query Match

Best Local Similarity 100.0%; Seed No. 1186-37; Matches 129; Conservative 0; Mismatches 0;

1276 CACGACGAGCTGATTAACAGCTTTCAGGCTATAGACATTAAGACCAAGCTGC 1335
121 CACGACGAGCTGATTAACAGCTTTCAGGCTATAGACATTAAGACCAAGCTGC 180
1336 CACGACGAGCTGATTAACAGCTTTCAGGCTATAGACATTAAGACCAAGCTGC 1395
181 CACGACGAGCTGATTAACAGCTTTCAGGCTATAGACATTAAGACCAAGCTGC 240
1396 CACGACGAGCTGATTAACAGCTTTCAGGCTATAGACATTAAGACCAAGCTGC 1404
241 CACGACGAGCTGATTAACAGCTTTCAGGCTATAGACATTAAGACCAAGCTGC 249

RESULT 9

AAZ74306
ID AAZ74306 standard; cDNA: 445 bp.

XX AAZ74306;

04-MAY-2001 (first entry)

Canine Interleukin-5 (IL-5) antibody: canine inhibitory immune response; immunoregulation; tumour; cancer; autoimmune disease; receptor; ss.

Canis sp.

W020011049 A2.

15-FEB-2001.

09-AUG-2000; 2000W-0527306.

10-AUG-1999; 99US-0087306.

(HESK-3) HESNA COKP

Gao H, Laxton R, Wondolting RS;

WP1: 2001-131542/1.

Novel canine Interleukin-5 (IL-5) antibody: canine inhibitory immune response; immunoregulation; tumour; cancer; autoimmune disease; receptor; ss. - claim 1; Page 35; 40pp; English.

The present invention provides the protein and nucleic acid sequences of canine Interleukin-5 (IL-5) and its ligand, thus can be used to treat or prevent response of Interleukin-5 allergies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used in detection, and in drug targeting.

UY 1276 CAGCAACCTCTGATTAAAGACCTTTCAGAGTAATACAGCATGAGACAGCAAGCTGGC 1345
 |||
 DB 76 CAGCAACCTCTGATTAAAGACCTTTCAGAGTAATACAGCATGAGACAGCAAGCTGGC 135
 |||
 UY 1346 CAGTGGAGAGCTGTGATTAACATATTCGAAACATTGTCTTAAIAAAGAGCAATATAG 1395
 |||
 DB 146 CAGTGGAGAGCTGTGATTAACATATTCGAAACATTGTCTTAAIAAAGAGCAATATAG 1395
 |||
 UY 1396 CAGTGGAGAGCTGTGATTAACATATTCGAAACATTGTCTTAAIAAAGAGCAATATAG 1395
 |||
 DB 196 CAGTGGAGAGCTGTGATTAACATATTCGAAACATTGTCTTAAIAAAGAGCAATATAG 1395
 |||

RESULT 10

AA150755

ID AA150755 standard: cDNA: 499 bp.

AC AA150755:

XX 24-SEP-1997 (first entry)

XX ovine IL-5 cDNA.

XX cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
 KW livestock; cow; stress; transport; vaccine adjuvant; early matu-
 KW cancer; immunosuppression; allergy; reproductive system; growth;
 KW early maturity; antibody; diagnosis; immunopotential;
 KW early hematopoietic precursor cells; cytokines; cells; lymphocytes;
 KW secretion; TCR; TGA; bacterial endotoxin; gamma interferon; SS.

XX ovine common alleles.

XX W09700421-A1.

XX 03-JAN-1997.

XX 14-JUN-1996; 96W0-A000400.

XX 27-OCT-1995; 95A0-0006244.

XX 14-JUN-1995; 95A0-0003502.

XX (CSTR) COMMANWEALTH SCI & IND RES OPI.

XX Sequ H. Wood P.

XX WPI: 1997 077528707.

XX P-PSDB: AAW08479.

XX Nucleotide acid encoding ovine interleukin-5 or -12 used as vaccine

XX adjuvants and to treat or prevent microbial infections in livestock

XX claim 6; Page 41-42; 78pp; English.

XX The sequences above in AA150755/56 encode ovine interleukin-5 (IL-5),
 XX ovine IL-5 or IL-12 are used to treat and/or prevent infections in
 XX livestock (esp. cows and sheep), particularly where the animals are
 XX stressed, e.g. during transport. IL-5 and IL-12 can also be used as
 XX adjuvants in vaccines for veterinary use (partic. weakly immunogenic
 XX subunit or synthetic peptide vaccines). They may also be used to
 XX treat cancer, immunosuppression and allergy, to enhance/suppress the
 XX reproductive system and to promote growth or early maturity. Optionally
 XX interleukin can be delivered from constructs or delivery cells and
 XX antibodies are useful in enzyme immunoassays for rapid diagnosis of
 XX infection. The interleukins are immunopotential, especially IL-5
 XX promotes growth of early hematopoietic progenitor cells and generation
 XX of cytotoxic cells from thymocytes, also it stimulates production and
 XX secretion of IgM and IgA (in synergism with bacterial endotoxin).
 XX IL-12 induces production of gamma-interferon by and proliferation
 XX of T and NK cells and increases the (non-specific) cytolytic
 XX lymphocyte response. The genetic constructs can also be used for
 XX in vitro production of IL-5 or -12.

SQ Sequence 499 BP; 130 A; 77 C; 94 G; 99 T; 0 other;

Query Match

Best local Similarity 2.6%; Score 48; 100 bp; Length 499;

Matches 43; Conservative 0; Mismatches 9; Gaps 0;

UY 100 CAGTGGAGAGCTGTGATTAACATATTCGAAACATTGTCTTAAIAAAGAGCAATATAG 142
 |||
 DB 68 CAGTGGAGAGCTGTGATTAACATATTCGAAACATTGTCTTAAIAAAGAGCAATATAG 110
 |||

RESULT 11

AA150755

ID AA150755 standard: DNA: 520 bp.

AC AA150755:

XX 24-SEP-1997 (first entry)

XX ovine IL-5 gene.

XX cytokine; ovine; sheep; interleukin-5; interleukin-12; IL-5; IL-12;
 KW livestock; cow; stress; transport; vaccine adjuvant; early matu-
 KW cancer; immunosuppression; allergy; reproductive system; growth;
 KW early maturity; antibody; diagnosis; immunopotential;
 KW early hematopoietic precursor cells; cytokines; cells; lymphocytes;
 KW secretion; TCR; TGA; bacterial endotoxin; gamma interferon; SS.

XX ovine common alleles.

XX W09700421-A1.

XX 03-JAN-1997.

XX 14-JUN-1996; 96W0-A000400.

XX 27-OCT-1995; 95A0-0006244.

XX 14-JUN-1995; 95A0-0003502.

XX (CSTR) COMMANWEALTH SCI & IND RES OPI.

XX Sequ H. Wood P.

XX WPI: 1997 077528707.

XX P-PSDB: AAW08479.

XX Nucleotide acid encoding ovine interleukin-5 or -12 used as vaccine

XX adjuvants and to treat or prevent microbial infections in livestock

XX claim 6; Page 49-50; 78pp; English.

XX The sequences above in AA150755/56 encode ovine interleukin-5 (IL-5),
 XX ovine IL-5 or IL-12 are used to treat and/or prevent infections in
 XX livestock (esp. cows and sheep), particularly where the animals are
 XX stressed, e.g. during transport. IL-5 and IL-12 can also be used as
 XX adjuvants in vaccines for veterinary use (partic. weakly immunogenic

and phosphorylated. The XhoI site within the first-strand synthesis primer was restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 400p cutoff, using a size-Sep 400 spun column from Pharmacia. The column eluent was then ligated into Stratagene's pBlueScript II KS+ predigested vector (pBlueScript II KS+) that had been digested with EcoRI and XhoI, and phosphorylated) with the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. This library was constructed by Dr. Paul Kelm and Dr. Virginia Corryell."

BASE COUNT 239 a 101 c 112 g 111 t 1 others

Query Match 1.68; Score 27; DB 10; Length 534;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 27; Conserved 0; Mismatches 0; Gaps 0;

QY 1458 TTTTCTTTTCTTTTACAGAGATT 1484
DB 184 TTTTCTTTTCTTTTACAGAGATT 158

RESULT 4
CNS04725 818 bp DNA Insert GSS 19-MAY-2000
DEFINITION Tetradon nigroviridis genome survey sequence PUC-ori of cDNA
084909 of library G from Tetradon nigroviridis, genome survey
sequence.

ACCESSION AL278618.1 GI:8014612
VERSION GSS: genome survey sequence.
KEYWORDS Tetradon nigroviridis.
SOURCE Tetradon nigroviridis.
ORGANISM Tetradon nigroviridis

REFERENCE 1 (bases 1 to 818)
Barnett, A., Filizadeh, C., Winkler, F., Bottling, P., Queller, F.,
Saurin, W., and Weissbach, J.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

TITLE Tetradon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 818)

AUTHORS Koest-Crollius, H., Jallion, O., Bastiva, O., Filizadeh, C., Fisher, C.,
Bonneau, L., Billault, A., Queller, F., Saurin, W., Barnett, A., and
Weissbach, J.
Characterization and repeat analysis of the compact genome of the
freshwater puterfish Tetradon nigroviridis

TITLE Unpublished
JOURNAL 4 (bases 1 to 818)

REFERENCE Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/16/T-tetra-pu/>

FEATURES
SOURCE Location/Qualifiers
1..818

contigname "Tetradon nigroviridis"
/db_xref="taxon:99883"
/cdate="080906"
/clone_lib="G"
/note="Genoscope genome survey of the PUC-ori"

BASE COUNT 192 a 185 c 189 g 246 t 5 others

Query Match 1.68; Score 27; DB 17; Length 818;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 27; Conserved 0; Mismatches 0;

QY 1449 CTCCTGCTCTTCTTTTCTTTTCTTTT 1475
DB 585 CTCCTGCTCTTCTTTTCTTTTCTTTT 611

RESULT 5
BE155390/c 129 bp cDNA

DEFINITION PM1-HT0350 270bp cDNA from H10350 Homo sapi
VERSION BE155390
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS

TITLE Shotgun sequencing of the human transcript
sequence 1005
PMID 10114044
PMID 10114044
COMMENT Laboratory of Human Genetics,
Ludwig Institute for Cancer Research,
Rui Proti, Avulso Institute 109, 4 andar,
Brazil

TEL: +55-11-2704742
FAX: +55-11-2704700
Email: asimpson@ludwig.org.br
This sequence was derived from the FAYESBY
Project. This entry can be seen in the
<http://www.ludwig.org.br/seq/seq.html>
300-010-096414 2000-04-27(4151)
Seq primer: puc 18 forward
High quality sequenced strand: 4
High quality sequenced strand: 68.

FEATURES
SOURCE Location/Qualifiers
1..129

ORGANISM "Homo sapiens"
/db_xref="taxon:9606"
/clone_lib "H10350"
/cdate "080459"
/dbstatus "Adult"

note "Human good luck! Vector:
Stratagene pBlueScript II KS+ was
derived from YESBRS PCR (G.S.)
No. 196-779. Ludwig Institute
profiles into the puc 18 vector
tissue mRNA and cDNA amplified
low stringency conditions."

BASE COUNT 42 a 27 c 33 t

Query Match 1.68; Score 26; DB 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 26; Conserved 0; Mismatches 0;

QY 1453 GCGCTCTTCTTTTCTTTTCTTTT 1478
DB 112 GCGCTCTTCTTTTCTTTTCTTTT 87

RESULT 6
B0022057 140 bp cDNA
F0022057

ORGANISM

Danio rerio
 Eukaryota; Metazoa; Chordata; Clariata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 Cyprinidae; Danio.

REFERENCE

1 (cases 1 to 322)
 Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kapra, L., Matlin, J., Beck, O., Wylic, J., Underwood, J., Stepien, M., Thomsen, B., Allum, M., Howers, Y., Person, B., Swiercz, T., Gibbons, M., Page, D., Harvey, N., Schark, R., Rittler, E., Koh, S., Shin, L., Jackson, Y., Chirbas, M., McGinn, K., Waterston, R., and Wilson, R.

TITLE

Washed zebrafish EST project 1998
 unpublished (1998)

JOURNAL

Contact: Stephen L. Johnson
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8001, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: zbratishewatson.wustl.edu
 The library was constructed by Dr. Z. Gong, JNA Sequencing by:
 Washington University Genome Sequencing Center St. Louis. Please
 contact Zhiyuan Gong for further information on this library
 (National University of Singapore, Department of Biological
 Sciences, Lower Kent Ridge Road, Singapore 119260).
 Seq primer: 14 bp from Amsterdam.

FEATURES

SOURCE

Location/Qualifiers

1..322
 /organism="Danio rerio"

/db="EST" "wustl" "955"

/clone="5154712"

/clone_11b "Gong zebrafish ovary"

/sex "female"

/dev_stage "4-5 month"

/db_host "MHLB (phase-resistant)"

/note "Gong ovary (fertilized); Vector: pTZ19; SK 1"

Site_1: XhoI; Site_2: EcoRI; Poly A: RNA was isolated from

the ovaries of 2 female adult zebrafish (4-5 month old).

cDNAs were made using oligo-dT primers and inserted into

lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo

mass-screened to places left SK following the Washington

University protocol

(http://jgscs.wustl.edu/seq/seq.html).

Please contact Zhiyuan Gong for further information on

this library (National University of Singapore,

Department of Biological Sciences, Lower Kent Ridge Road,

Singapore 119260)."

BASE COUNT

115 a 48 c 59 g 99 t

ORIGIN

Query Match

Best Local Similarity 1.68; Score 26; DB 13; Length 322;

Matches 26; Conservative 0; Mismatches 0; Indels 0;

QY 1457 GTTTTTTTTTTTTACACAAA 1482

146 GTTTTTTTTTTTTACACAAA 291

Search completed: November 8, 2002, 06:05:59
 Job time: 3082.49 secs

NAME: MURPHY, KATE H
REGISTRATION NUMBER: 29,759
REFERENCE CHECK NUMBER: 29,759
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1508
TELEFAX: 202-882-0168
TELEX:
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 base pairs
TYPE: double-stranded
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: Aspergillus niger
STRAIN: N430
INSTRUMENTAL IS DATA: CBS120.49
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 57..273
OTHER INFORMATION: product "cellulase"
US 09-478-816-1

Query Match: 148, Score 23, DB: 1, Length 107,
Post Local Similarity: 100.0%, Prod. No. 1,67
Matches: 27, Mismatch: 0, Mismatch: 0, Indel: 0, Gap: 0
DB: 1458 TTTTCTTTTCTTTTACAG 1480
111111111111111111111111
DB: 1010 TTTTCTTTTCTTTTACAG 988

RESULT 9

Sequence 257: Application US/09146476
Patent No. 6,420,526
GENERAL INFORMATION:
APPLICANT: ROSEN, et al.
TITLE OF INVENTION: 186 Human Secreted Proteins
FILE REFERENCE: P200201
CURRENT ATTENTION NUMBER: 60/047,592
EARLIER ATTENTION NUMBER: 1997-05-24
EARLIER ATTENTION NUMBER: 1998-04-06
EARLIER ATTENTION NUMBER: 60/047,592
EARLIER ATTENTION NUMBER: 1997-04-07
EARLIER ATTENTION NUMBER: 60/040,433
EARLIER FILING DATE: 1997-04-07
EARLIER APPLICATION NUMBER: 60/049,422
EARLIER FILING DATE: 1997-04-07
EARLIER APPLICATION NUMBER: 60/049,426
EARLIER FILING DATE: 1997-04-07
EARLIER APPLICATION NUMBER: 60/049,434
EARLIER FILING DATE: 1997-04-07
EARLIER APPLICATION NUMBER: 60/049,436
EARLIER FILING DATE: 1997-04-07
EARLIER APPLICATION NUMBER: 60/049,438
EARLIER FILING DATE: 1997-04-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,697
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,702
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,743
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,793
EARLIER FILING DATE: 1997-05-24

EARLIER APPLICATION NUMBER: 60/047,617
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,618
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,561
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,584
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,500
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,587
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,492
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,598
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,613
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,592
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,692
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-24
EARLIER APPLICATION NUMBER: 60/047,580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,569
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EARLIER FILING DATE: 1997-04-11
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EARLIER APPLICATION NUMBER: 60/047,674
EARLIER FILING DATE: 1997-04-11
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,615
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,974
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EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 08:51:15 ; Search time 1703.89 seconds

(without alignments)
10260 168 Million cell updates/sec

Title: US-09-755-633-18

Perfect score: 1658

Sequence: 1 aggaacacacgaacatc.....tattggaagatttggaga 1658

Scoring table: OLIGO_NOC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4105280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: listing first 45 summaries

Database :

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11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: gb_da:*

16: gb_fun:*

17: gb_hum:*

18: gb_in:*

19: gb_mu:*

20: gb_cm:*

21: gb_ov:*

22: gb_pat:*

23: gb_ph:*

24: gb_pl:*

25: gb_pr:*

26: gb_ro:*

27: gb_sts:*

28: gb_sy:*

29: gb_un:*

30: gb_vl:*

31: gb_da:*

32: gb_fun:*

33: gb_hum:*

34: gb_in:*

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36: gb_cm:*

37: gb_ov:*

38: gb_pat:*

39: gb_ph:*

40: gb_pl:*

41: gb_pr:*

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the
and is derived by analysis of the total score of

SUMMARIES

Result No.	Score	Query Match	Length	Id	
1	1658	100.0	1658	4	AF331920
2	170	10.3	620	4	AF331919
3	144	8.7	405	4	AX083939
4	129	7.8	445	4	AX083948
5	129	7.8	556	4	AF091183
6	43	2.6	520	4	AF085938
7	42	2.5	1310	4	U01101
8	42	2.5	1305	4	SC011098
9	42	2.5	629	4	SC013452
10	41	2.5	405	4	AF088770
11	41	2.5	405	4	B11811E05
12	41	2.5	608	4	AF125436
13	39	2.4	405	4	AF091947
14	30	1.8	404	4	AF051472
15	29	1.7	174446	4	AF160491
16	29	1.7	20912	4	AF084146
17	28	1.7	405	4	AF294756
18	28	1.7	504	10	U0184588
19	28	1.7	162084	4	AF005962
20	27	1.6	186174	4	AF086225
21	27	1.6	186000	4	AF099750
22	26	1.6	740	4	AX182851
23	26	1.6	997	10	B019768
24	26	1.6	1562	9	B0001555
25	26	1.6	4845	4	AX149445
26	26	1.6	2815	4	U0118244
27	26	1.6	3236	4	AF146275
28	26	1.6	3230	4	B005640
29	26	1.6	4230	4	B14592
30	26	1.6	4230	4	BSE-D1PE1
31	26	1.6	4230	4	H08115
32	26	1.6	4241	9	H08115A
33	26	1.6	4537	9	BH8211C942
34	26	1.6	4537	9	BH8211C942
35	26	1.6	57146	9	AF004042
36	26	1.6	59605	9	AF108221
37	26	1.6	92462	4	AF010560
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39	26	1.6	128768	4	AF112679
40	26	1.6	149945	9	AF1160398
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42	26	1.6	18042	4	AF079320
43	26	1.6	19242	4	AF090803
44	26	1.6	19285	4	AF115466
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ALIGNMENTS

RESULT 1

AF331920

LOCUS AF331920

DEFINITION Canis familiaris Interleukin-5 gene, 1558 bp, JNA

ACCESSION AF331920

VERSION AF331920.1 GI:1593182

KEYWORDS

SOURCE

ORGANISM

Canis familiaris.

Canis familiaris.

Eukaryota; Metazoa; Mammalia; Eutheria; Carnivora; Fissipedia

Mammalia; Eutheria; Carnivora; Fissipedia

1 (bases 1 to 1558)

Yang, S., Solinus, K.S., Weber, E., and Mital

Canine Interleukin 5 molecular characterization

Expression of Interleukin 5 and its receptor



PN EP261625-A.
 XX 30-MAR-1988.
 XX 21-SEP-1987; 87EP-011377A.
 XX 20-SEP-1985; 86JP-0223284.
 PA (HONJ/) HONJO T.
 PA Honjo T., Takatu K., Severinson E.
 XX WPI: 1988-085927/13.
 DR P-F5DB, AAF81056.
 XX Recombinant human B cell differentiation factor
 PI used for diagnosis or treatment of immuno deficiency diseases,
 PT various infections and cancers
 XX
 XX Example: Fig 5(1) 5(4); 35pp; English.
 XX
 XX Nucleotide sequence of the exon portions of the human B220 chromosomal
 CC gene completely coincided with the nucleotide sequence of human BCP
 CC cDNA (JAN81380). The BCP is useful in the diagnosis or treatment of
 CC e.g. immunodeficiency diseases occurring due to the deficiency of this
 CC factor in a living body and also in the treatment of various infections
 CC and cancers.
 XX
 XX Sequence 1230 RP; 1027 A; 545 C; 622 G; 1036 T; 0 other;
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 Matches 1212; Conservative 0; Mismatches 384; Indels 191; Gaps 19;
 QY 1 AGGCAACACCTGACATTCATGAGTATGAGAAAGCTGCTATTTGGTGTACTG 69
 DB 527 AGGCAACACCTGACATTCATGAGTATGAGAAAGCTGCTATTTGGTGTACTG 586
 QY 61 TGGGCGCTGGGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 DB 587 TGGGCGCTGGGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 645
 QY 121 AGGCGTGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
 DB 647 AGGCGTGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 706
 QY 181 TTTTGATTCCTACAGTCTTAAAGATGAGGCTATGCTGCTGCTGCTGCTGCT 234
 DB 707 TTTTGATTCCTACAGTCTTAAAGATGAGGCTATGCTGCTGCTGCTGCTGCT 766
 QY 235 -TTTAAAGATGCTATTCATTAATGAAGTACAGTCTTAAATATATATATGCTGCT 293
 DB 767 ATATAGAGATGCTTAAATATGAATTAAGATTCGAG-CACATTAAGTACAGCGGTGATTAAGT 825
 QY 294 ATGTATCTGAGAAATATATATTAAGATTAAGCTTACATATCATATTAAGTAAATG 353
 DB 826 ACATGACACGACAAACATCTGCTTAAAGATTAAGTACAGTGTGCTGCTGCTGCTGCT 885
 QY 354 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 413
 DB 886 -TATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 944
 QY 414 AATATATGATTTGATTAAGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGT 469
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 DB 1005 TCAATATGATTTGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGT 1064
 QY 530 AATATGATTTGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGT 588
 DB 1065 GAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1109

QY 589 GAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 647
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 DB 1284 AGGCGTGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 828
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 DB 1343 -CTATATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGTATTAAGT 888
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GenBank version 5.1.4
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QM nucleotide nucleotide search using SW model

Run on: November 7, 2002, 08:51:15, Search time 4704.17 seconds

(without alignment)
10259.568 Million cell updates/sec

Title: US-09-755-633-18

Perfect score: 14551402878 (without alignment)

Sequence: 14551402878

Scoring table: IDENTITY-MD

Gapop 10.0, Gapext 1.0

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match: 98
Maximum Match: 1000
Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a

score greater than 14551402878, the score of the
and is derived by multiplying the total score by

RESULTS

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4	634.6	38.3	AF331920	4	634.6
5	634.6	38.3	AF331920	4	634.6
6	634.6	38.3	AF331920	4	634.6
7	600.6	36.2	AF331920	4	600.6
8	600.6	36.2	AF331920	4	600.6
9	600.6	36.2	AF331920	4	600.6
10	600.6	36.2	AF331920	4	600.6
11	599	36.1	AF331920	4	599
12	490.6	29.6	AF331920	4	490.6
13	347.4	21.0	AF331920	4	347.4
14	272.6	16.4	AF331920	4	272.6
15	245.2	14.8	AF331920	4	245.2
16	221.6	13.4	AF331920	4	221.6
17	216	13.0	AF331920	4	216
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1140643
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Yano, S.
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Project Parkway, W. Collins, CO 80521, USA
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/db_xref "GI:15919183"
/translation "MPELNLSTLALAAVSAVAVENMNLVASELELSINHLPL
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DB 61 TGGGATGCTTAAGTTCTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTT 120
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DB 1441 TTTGATTCCTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTT 1500
QY 1501 TTTGATTCCTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTT 1560
DB 1501 TTTGATTCCTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTT 1560
QY 1561 TTTGATTCCTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTT 1620
DB 1561 TTTGATTCCTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTT 1620
QY 1621 TTTGATTCCTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTT 1680
DB 1621 TTTGATTCCTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTTAAAGCTTT 1680

RESULT 2


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UY 201 AAAATCATGGGTAATGGTGGCGGCGGACTG-----TTTAAATGATGATTGCA 254
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DB 1 AAAATCATGGGTAATGGTGGCGGCGGACTGTTAATAATAATAATAATCTGGTAATA 60
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UY 254 TAAATGAAATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 314
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DB 61 TAAATGAAATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 119
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UY 414 ATTAATAATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 373
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DB 120 GTTAATAATGATGATGATGATTAATTAATAATAATAATAATAATAATAATAATA 178
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UY 474 AATTAATGATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 433
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UY 490 GATTAATGATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 548
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DB 299 TATTAATGATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 358
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UY 549 AATTAATGATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 608
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UY 609 TATTAATGATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 668
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DB 404 TATTAATGATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 462
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DB 463 TATTAATGATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 520
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UY 729 TATTAATGATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 788
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DB 521 TATTAATGATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 577
    1111111111111111111111111111111111111111111111111111111
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UY 756 TATTAATGATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 807
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DB 1029 TATTAATGATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 1088
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UY 808 TATTAATGATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 867
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DB 1089 AATTAATGATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 1147
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UY 984 AATTAATGATGATGATGATTAATTAATAATAATAATAATAATAATAATAATAATA 1043
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DB 1104 GATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1162
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UY 1277 GATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1336
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DB 1163 GATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1222
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RESULT 13
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 VERSION
 017052.1 GI:897558
 KEYWORDS
 1 of 2
 SHEEP
 ORGANISM
 Sheep
 Ovis aries
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Laurasiatheria; Artiodactyla;
 Ruminantia; Pecora; Bovidae;
 Bovidae; Caprinae; Ovis;
 1 (bases 1 to 1140)
 REFERENCE
 1 Bryson C.E., Viney E., Brandon M. and Boyd A.W.
 Duplication of the sheep Interlookin-5 gene
 2 (bases 1 to 1140)
 REFERENCE
 1 Bryson C.E.
 Direct Submission
 Submitted (08-NOV-1994) Claitor E. Bryson, Department of Veterinary
 Science, University of Melbourne, Flemington Rd., Parkville,
 Victoria, 3052, Australia
 Location/Qualifiers
 1..1140
 Organism: Ovis aries
 db_xref: taxon:9940
 339..347
 /gene="IL5"
 349..356
 /gene="IL5"
 470..607
 /gene="IL5"
 /number=1
 824..856
 /gene="IL5"
 /number=2


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PRIOR APPLICATION DATA:
AFFILIATION NUMBER: 09-APR-1997
FILING DATE: 09-APR-1997
ATTORNEY AGENT ID# AAAAGH
NAME: VIKSITUS, Ann S
REGISTRATION NUMBER: 37,746
REFERENCE/CLASS# NUMBER: 156,16708Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-3260
TELEFAX: 612-339-3061
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1534 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURES:
NAME/KEY: Ref_Protein
LOCATION: 104..442
OTHER INFORMATION:
US 09-156-864 4

Query Match:
Post Local Similarity: 5.3%; Score 87.2; DB 4; Length 1534;
Matches 104; Conservation: 0; Mismatches 28; Indels 0; Gaps 0;

UY 1274 AATGTAACCTGGTGTATAAACAAGTTTCAGCGATATGAAGAAAGCAAAAACCTC 1033
DB 216 ATGATCAAATATCATATCAAGAACTTTCAAGAGCTATGAATATGAAGAAAGCAAAAACCTC 275

UY 1334 CTAACGACGAGATGTCGATTAACACTTATTCAAAACCTTGCTTTTATATAAACACACATAC 1393
DB 275 CTCTCCGCTGATATGCGCAAACTTATTTTAAAACTGTATGATGAAGAAAGCAAAAACCTC 405

UY 1394 AGCGGCAAAAAG 1405
DB 336 AGCGGCAAAAAG 447

RESULT 9
US 09-160-864-1
Sequence 1: Application US/09180864
Patient No. 6465616
GENERAL INFORMATION:
APPLICANT: Joseph, AnneJ
APPLICANT: Vasas, Matthew
APPLICANT: Shannon, Frances
APPLICANT: Bastiras, Stan
APPLICANT: Hey, Allan W
TITLE OF INVENTION: AN INTERFERIN C ANTAGONIST
FILE REFERENCE: 99/22
CURRENT APPLICANT NUMBER: 99999766-564
CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 08/591,498
PRIOR FILING DATE: 1994-07-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: patent Ver. 2.1
SEQ ID NO: 1
LENGTH: 477
TYPE: DNA
ORGANISM: nucleotide sequence encoding modified IL-5
FEATURES:
NAME/KEY: IL-5
LOCATION: (4)..(466)
US 09-160-864 1

Query Match:
Post Local Similarity: 5.1%; Score 85.2; DB 4; Length 377;
Matches 102; Conservation: 0; Mismatches 28; Indels 0; Gaps 0;

UY 1274 AATGTAACCTGGTGTATAAACAAGTTTCAGCGATATGAAGAAAGCAAAAACCTC 1333

```

[illegible]

Sequence 651, Application US/69641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Maria
APPLICANT: Bouguetel, Joëlle
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Amichai
TITLE OF INVENTION: PHYLIC MAPING METHOD FROM GENOMIC PROTEOUS CAPTURE
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET, 0510P1
CURRENT APPLICATION NUMBER: us 09/775,267
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: us 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: us 60/775,267
PRIOR FILING DATE: 1999-05-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pat
SEQ ID NO 651
LENGTH: 20674
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1123..4123
OTHER INFORMATION: 5' regulatory region
NAME/KEY: exon
LOCATION: 4124..3297
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 3871..1072
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 5552..5633
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 5749..5880
OTHER INFORMATION: exon 4
NAME/KEY: exon
LOCATION: 5936..6039
OTHER INFORMATION: exon 5
NAME/KEY: exon
LOCATION: 6147..6505
OTHER INFORMATION: exon 6
NAME/KEY: exon
LOCATION: 7379..7522
OTHER INFORMATION: exon 7
NAME/KEY: exon
LOCATION: 8645..8854
OTHER INFORMATION: exon 8
NAME/KEY: exon
LOCATION: 12254..12340
OTHER INFORMATION: exon 9
NAME/KEY: exon
LOCATION: 12954..13023
OTHER INFORMATION: exon 10
NAME/KEY: exon
LOCATION: 13108..13429
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NAME/KEY: exon
LOCATION: 16567..16667
OTHER INFORMATION: exon 12
NAME/KEY: exon
LOCATION: 16775..16945
OTHER INFORMATION: exon 13
NAME/KEY: exon
LOCATION: 17063..17554
OTHER INFORMATION: exon 14
NAME/KEY: misc_feature

LOCATION: 17555..20674
OTHER INFORMATION: 3' regulatory region
NAME/KEY: allele
LOCATION: 1128
OTHER INFORMATION: 1128 polymorphic base
NAME/KEY: allele
LOCATION: 1182
OTHER INFORMATION: 1182 polymorphic base
NAME/KEY: allele
LOCATION: 1559
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NAME/KEY: allele
LOCATION: 1570
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LOCATION: 2323
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NAME/KEY: allele
LOCATION: 6183
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NAME/KEY: allele
LOCATION: 6338
OTHER INFORMATION: 6338 polymorphic base
NAME/KEY: allele
LOCATION: 6375



[illegible]

RESULTS	997 bp	EMA	11000	358 M	99.1%
CONSOLIDATED					
LOCUS	CONSOLIDATED				
DEFINITION	Protophila melanogaster genome survey sequence, site 62 of 1000				
	11000				
	11000				
ACCESSION	U000000000				
VERSION	1.0				
KEYWORDS	Protophila melanogaster				
	Protophila melanogaster				
ORGANISM	Protophila melanogaster				

REFERENCE	1 (bases 1 to 987)
AUTHORS	Genoscopy
TITLE	Direct Submission
JOURNAL	Submitted (23 JUL 1999) at Genoscopy - Centre National de Recherche

COMMENT
collaboration of this RAG-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <http://www.odip.ch/edgp/> - This Drosophila melanogaster RAG library (Ipsos RAG) was made by Alain Palland at OIEB (Centre d'Etude du Polymorphisme Humain) with funding provided by a MEC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

FEATURES
Location/Qualities
1997

[illegible]

Query Match	4.18	Score 67.21	DB 17	Length 987
Best Local Similarity	22.48	Prod. No. 0.853		
Matches	94	Conservative	122	Indels 0
		Mismatches	122	Gaps 0

97 1122 ATATTTTATTCTCCACATAAAANV DAAVTACTATAAATTAAGTCGCAATGTAA 1161
 | :| : | :| :||| ||| : | :||
Lib 986 AAAAAATAAACCTCMMMAAMTTMAAAAAAAAAAAAHHHWWWWWTTTTTTTTTTTT 927

09 1182 CUGATACCTTAAGCTTAAATAATGCAAGTCATCATGTGAATCATTTATATCAATCATPRA 1241
| : ||| : : : | : : | : : | : : | : : |
726 TTAAGWTITAAWIMWWWHWTITYHWWWWIWIITINNAITWTTITWATITWIMAWCYCYNIA 867

DDB

GY 1362 CATGGTTACCATTTTATATATTAAAGCACTGACTTCATTATTCATA 1411
 ||||| : | | | - | : : : : |
Ddb 746 WWTAAAWMTTKTTTTWTTTAAAAAANNNNNAWWMAAWMAANN 697

RESD1.6	1101 bp	JUN-03-JUN-1999
CNS004YC		
LOCUS		
DEFINITION	CNS004YC melanin cluster sequence (Locus of HMC2)	
	HMC2/2804 of RPEC-98 library from <i>Protophila melanogaster</i> (fruit fly)	
ACCESSION	1101 genomic survey sequence.	
	A071206	

[illegible]

JOURNAL submitted (02-JUN 1999) Genoscope, Centre National de Séquençage 1
BP 101 51006 EVRY-COURCOURA FRANCE (E-mail: a.sorci@genoscope.cns.fr)
Web: www.genoscope.cns.fr
acceptation of this bioRx preprint was certified out as part of a
COMMITMENT

Dr. Jeanne Messemmer in French de Jond's laboratory in the Department of Clinical Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI 96 and was constructed by partial EcoRI digestion of prothoplast DNA provided by the RMP1 from the isogenic strain Y2, cv. bw sp. The same strain used for the Burt's #1 and Est. libraries was more detailed description of the library and how to order individual PAC clones. The entire library of 1118 for hybridization from the RMPAC Resource Center can be found at <http://labpac.med.buffalo.edu/protoplast.html>.

PLATONIS	LOCATION/QUALIFIERS
SOURCE	1. 1101

Query Match	Score	Length
Best Local Similarity	42.5%	1101
	Pred. No. 0.0977	
Sequence	66.25	148
Protein	102.5	177
Origin	128.5	194

[illegible]

1207 AACCTATCATCTAATCATTTTATCAAAATCAATATTTACTTACATTTTAAATTTCAGS 1266

1267 AATGACATCATAGGTTCATAAAAGAAAAGAAATACCATTCATTTAATATATATGTA 1326
+ : + : + : + : + : + : + : + : + : + : + : + : + : + : + : +

[illegible][illegible]

[illegible][illegible]





Genome version 5.1.3
Copyright (c) 1993 - 2002 CompuLink Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 08:51:15 : Search time 4763.17 Seconds

(without alignment)
10256 568 Million cell updates/sec

File: US-09-755-633-19

Port score: 1658

Sequence: 1 to 568 nucleotides (100% identity) (100% identity)

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Search: 2054640 seqs, 14551402879 positions

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2080000000

Post processing: Minimum Match 98

Maximum Match 100

Listing first 45 similarities

Database:

1: qb_ba:*

2: qb_ba:*

3: qb_ba:*

4: qb_ba:*

5: qb_ba:*

6: qb_ba:*

7: qb_ba:*

8: qb_ba:*

9: qb_ba:*

10: qb_ba:*

11: qb_ba:*

12: qb_ba:*

13: qb_ba:*

14: qb_ba:*

15: qb_ba:*

16: qb_ba:*

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37: qb_ba:*

38: qb_ba:*

39: qb_ba:*

40: qb_ba:*

41: qb_ba:*

pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the
and is derived by dividing 1 by the total score of

REMARKS

Result No.	Score	Query Match	Query Length	Hit
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3	623.6	47.6	1000	AF331920
4	623.6	47.6	1000	AF331920
5	623.6	47.6	1000	AF331920
6	623.6	47.6	1000	AF331920
7	589.6	45.6	1000	AF331920
8	589.6	45.6	1000	AF331920
9	589.6	45.6	1000	AF331920
10	589.6	45.6	1000	AF331920
11	589.6	45.6	1000	AF331920
12	481.2	29.0	1000	AF331920
13	481.2	29.0	1000	AF331920
14	481.2	29.0	1000	AF331920
15	265.2	16.0	1000	AF331920
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17	265.2	16.0	1000	AF331920
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ALIGNMENTS

RESULT 1
AF331920
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
expression of the gene

REFERENCE 1 (bases 1 to 450)
 AUTHORS Bryson, C.E., Viner, E., Braden, M., and Boyd, A.W.
 TITLE Structure of the sheep interleukin-5 gene
 JOURNAL Immunol
 REFERENCE 2 (bases 1 to 450)
 AUTHORS Bryson, C.E.
 TITLE Direct Submission
 JOURNAL Submitted (08 Nov 1994) Claire E. Bryson, Department of Veterinary
 Science, University of Melbourne, Flemington Rd., Parkville,
 Victoria, 3052, Australia

FEATURES
 SOURCE location/qualifiers
 1..450

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ORIGIN /gene "IL5"
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 268..366)
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 join(017052.1:479..467,017052.1:824..856,42..460,268..466)
 /gene "IL5"

ORIGIN /protein "Interleukin-5"
 /protein_id="AA860629.1"
 /db_xref="GI:897561"
 /translation "MKAELLVANLAAVYLAHVESTRMLVATLLISTHOTLLG
 DNNMLTPTHTHCCTETVCTFGLFNGVAGLEAVKELEPRLSLEAYELQTRF
 CQGRMRKQPLLYLOVHGLVINTFMES"

ORIGIN /gene "IL5"
 /number=3
 268..366
 /gene "IL5"
 /number=4

ORIGIN /number=4
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 72..C 99..4 142..1

ORIGIN /number=4
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 72..C 99..4 142..1

ORIGIN /number=4
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 72..C 99..4 142..1

ORIGIN /number=4
 147..472
 72..C 99..4 142..1

ORIGIN /number=4
 147..472
 72..C 99..4 142..1

ORIGIN /number=4
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 72..C 99..4 142..1

ORIGIN /number=4
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 72..C 99..4 142..1

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 72..C 99..4 142..1

ORIGIN /number=4
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 72..C 99..4 142..1

ORIGIN /number=4
 147..472
 72..C 99..4 142..1

ORIGIN /number=4
 147..472
 72..C 99..4 142..1

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 72..C 99..4 142..1

ORIGIN /number=4
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 72..C 99..4 142..1

ORIGIN /number=4
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 72..C 99..4 142..1

ORIGIN /number=4
 147..472
 72..C 99..4 142..1

ORIGIN /number=4
 147..472
 72..C 99..4 142..1

ORIGIN /number=4
 147..472
 72..C 99..4 142..1

ORIGIN /number=4
 147..472
 72..C 99..4 142..1

ORIGIN /number=4
 147..472
 72..C 99..4 142..1

ORIGIN /number=4
 147..472
 72..C 99..4 142..1

ORIGIN /number=4
 147..472
 72..C 99..4 142..1

ORIGIN /number=4
 147..472
 72..C 99..4 142..1

ORIGIN /number=4
 147..472
 72..C 99..4 142..1

ORIGIN /number=4
 147..472
 72..C 99..4 142..1

and phosphorylated. The XhoI site within the first strand synthesis primer was restricted by digestion with XhoI.

all XhoI sites in the cDNA would be protected by their hometylated status. The cDNA construct is a size-fractionated with a 400bp cutoff, using a SicoSep 400 spin column from Pharmacia. The column eluent was then ligated into Stratagene's pBluescript II SK(+) XhoI digested vector (pBluescript II SK(+)) that had been digested with XhoI and XhoI, and phosphorylated. Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts. This library was constructed by Dr. Paul Klem and Dr. Virginia Corryell.

BASE COUNT 209 a 101 c 112 g 111 t 1 others

Query Match 1.6% Score 27; DB 10; Length 534;
Host Local Similarity 100.0%; Prod. No. 0;
Matches 27; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 AATCTTGTATATAAAAAAAAAAAAAA 201
DB 158 AATCTTGTATATAAAAAAAAAAAAAA 184

RESULT 4
CNS04725/c 818 bp DNA linear GSS 19-MAY-2000
DEFINITION Tetradon nigroviridis genome survey sequence for 31 end of clone
sequence.

ACCESSION AL278618.1 GI:8014612
KEYWORDS GSS: genome survey sequence;
ORGANISM Tetradon nigroviridis;
Tetradon nigroviridis;
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetradoniformes;
Tetradontidae; Tetradon;
1 (bases 1 to 818)

REFERENCE 1 (bases 1 to 818)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 2 (bases 1 to 818)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 3 (bases 1 to 818)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 4 (bases 1 to 818)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 5 (bases 1 to 818)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 6 (bases 1 to 818)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 7 (bases 1 to 818)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 8 (bases 1 to 818)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 9 (bases 1 to 818)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

BASE COUNT 192 a 185 c 189 g 246 t 5 others
ORIGIN 1.6% Score 27; DB 17; Length 818;
Query Match 1.6% Score 27; DB 17; Length 818;

Host Local Similarity 100.0%; Prod. No. 0;
Matches 27; Conservation 0; Mismatches 0;

QY 124 AAAAAAAAAAAAAAAAAAAAAAA 210
DB 611 AAAAAAAAAAAAAAAAAAAAAAA 210

RESULT 5
B0022057/c 140 bp mRNA
DEFINITION Human
ACCESSION B0022057.1 GI:8014612
KEYWORDS EST;
SOURCE human;
ORGANISM Homo sapiens;
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetradoniformes;
Tetradontidae; Tetradon;
1 (bases 1 to 140)

REFERENCE 1 (bases 1 to 140)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 2 (bases 1 to 140)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 3 (bases 1 to 140)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 4 (bases 1 to 140)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 5 (bases 1 to 140)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 6 (bases 1 to 140)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 7 (bases 1 to 140)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 8 (bases 1 to 140)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 9 (bases 1 to 140)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 10 (bases 1 to 140)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 11 (bases 1 to 140)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 12 (bases 1 to 140)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 13 (bases 1 to 140)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 14 (bases 1 to 140)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

REFERENCE 15 (bases 1 to 140)
Korostoff, J. S., Gill, J. C., Pappas, C. E., Fisher, C. E.,
Korostoff, J. S., Pappas, C. E., Pappas, C. E., Pappas, C. E.,
Saurin, W. and Weissbach, J. L.
Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence

BASE COUNT 42 a 27 c 27 g 112 t 1 others
ORIGIN 1.6% Score 27; DB 17; Length 818;
Query Match 1.6% Score 27; DB 17; Length 818;
Host Local Similarity 100.0%; Prod. No. 0;
Matches 27; Conservation 0; Mismatches 0;

QY 191 TTTTAAAAAAAAAAAAAAAAAAAA 206
DB 87 TTTTAAAAAAAAAAAAAAAAAAAA 206

RESULT 6
B0022057/c 140 bp mRNA
DEFINITION Human
ACCESSION B0022057.1 GI:8014612
KEYWORDS EST;
SOURCE human;
ORGANISM Homo sapiens;
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetradoniformes;
Tetradontidae; Tetradon;
1 (bases 1 to 140)

[illegible][illegible]

REFERENCE 1 (bases 1 to 202)
 AUTHORS Bonaldi,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 COMMENT 9794447
 contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 3565
 Email: msoares@uiowa.med.uiowa.edu

FEATURES
 source
 location/Accession:iers
 1..202
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /cdate="01-R-800" 9 12 0 01"
 /cdate="01-R-800"
 /cdate="01-R-800"
 /dev_stage="adult"
 /lab_host="DH10b (Life Technologies)"
 /note="Vector pV14-4 (Pharmacia) with a modified polylinker site. Not a site. Dec 91. The library (01-R-800) is a subtracted library derived from a mixture of the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cortex, corpus striatum and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratlist.eng.uiowa.edu. The subtraction has been previously described in (Bonaldi, Lennon and Soares, Genome Research 6:791-806, 1996)
 TAGLIB=01-R-800
 TAG_TISSUE=cerebellum
 TAG_SEQ_CGCAC"

BASE COUNT 56 a 40 c 35 g 21 t

Query Match 1.5% Score 26; DB 10; Length 202;
 Best Local Similarity 100.0%; Prod. No. 0;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Y 175 AATCTGTAAAAA 200
 DB 26 AATCTGTAAAAA 1

RESULT 9
 AA475229 225 bp mRNA 11base EST 19 JUN 1997
 LOCUS 21402.F1 Soares mammary gland_NbMm Mus musculus cDNA clone
 DEFINITION IMAGE:875403 5', mRNA sequence.
 ACCESSION AA475329
 VERSION AA475329.1 01:000000
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Chordata; Granulata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 202)
 REFERENCE
 AUTHORS Maria M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dombrowski, T.,

TITLE
 JOURNAL
 COMMENT
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Maria M. at 319 335 8250
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 444 Forest Park Library, Box 8501, St. Louis
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.wustl.edu
 This clone is available royalty-free from
 IMAGE Consortium (<http://image.llnwd.net>) for
 MGI:514883
 Seq Primer: -2000 + 1000 bp from Amino Acid
 High quality sequence shop: 110.

FEATURES
 source

location/Accession:iers
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 /organism="Mus musculus"
 /strain="FVB/NJ"
 /db_xref="taxon:10090"
 /cdate="MARCH 95/03"
 /cdate="MARCH 95/03"
 /cdate="MARCH 95/03"
 /dev_stage="adult"
 /lab_host="DH10b"
 /note="mammary gland; Vector pV14-4 (Pharmacia) with a modified polylinker site. Not a site. Dec 91. The library (01-R-800) is a subtracted library derived from a mixture of the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cortex, corpus striatum and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratlist.eng.uiowa.edu. The subtraction has been previously described in (Bonaldi, Lennon and Soares, Genome Research 6:791-806, 1996)
 TAGLIB=01-R-800
 TAG_TISSUE=cerebellum
 TAG_SEQ_CGCAC"

BASE COUNT 88 a 40 c 43 g 31 t

Query Match 1.5% Score 26; DB 10; Length 202;
 Best Local Similarity 100.0%; Prod. No. 0;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Y 181 AAAAAA 277
 DB 104 AAAAAA 179

RESULT 10
 B6651868 271 bp mRNA
 LOCUS B6651868
 DEFINITION ID: B6651868.1 01:000000
 ACCESSION B6651868.1 01:000000
 VERSION B6651868.1 01:000000
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max.
 Eukaryota; Viridiplantae; Streptophyta; Euphorbiales; Fabales; Fabaceae; Leguminosae; Rosales; eudicotyledons; Fabales; Fabaceae; Leguminosae; Glycyne.
 1 (bases 1 to 271)
 REFERENCE
 AUTHORS Shoemaker, P., Krom, L., Winkler, L., Hildebrand, A., Bolla, B., Maria, M., Hillier, L., Kent, W., Ylitalo, J., Hunkeler, K., Stoeckert, M., Kent, A., Peterson, B., Swafford, J., Oldham, R., P., Elliot, E., Kohn, S., Shio, T., Johnson, J.R., Waterston, R., and Wilson, R.

TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/2444 Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63109, USA
TEL: 314 286 1800
FAX: 314 286 1810
Email: est@wustl.edu

FEATURES
SOURCE
1..271
/organism="Medicago truncatula"
/db_xref="taxon:4880"
/clone="NF091H021R"
/tissue_type="seedlings"
/dev_stage="seedling"
/notes="Vector: Lambda ZAP. Specimens were prepared either by 100 Gy gamma or 0.5, 1, 5, or 10 kGy UV irradiation. Gamma-irradiated samples were harvested at 4, 12, 24 and 48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. RNA was prepared from poly(A⁺) enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directly ligated into the Uni-ZAP-XR vector (Stratagene) and packaged using the Gigapack III packaging extracts. Plasmids containing cDNA inserts were purified and excised from the recombinant DNA ZAP-XR vector using Fastap (PharMingen) and the PstI-XbaI strain XL1-Blue MRF⁺ (Stratagene). Excised plasmids were plated using SOB+ cells."

QUERY MATCH
Best local similarity 100.0% Ident. No. 0
Matches 26 Overlapped 0 Mismatches 0 Indels 0 Gaps 0

Y 176 ATCTCTTAAAAA
|||||
DB 217 ATCTCTTAAAAA
|||||

BASE COUNT
124 a 48 c 44 g 76 t

ORIGIN
1..693 Score 26 DB 12 Length 271
Best local similarity 100.0% Ident. No. 0
Matches 26 Overlapped 0 Mismatches 0 Indels 0 Gaps 0

Y 176 ATCTCTTAAAAA
|||||
DB 217 ATCTCTTAAAAA
|||||

RESULT 11
H0156344
CORGUS
DEFINITION
NE091H021R1094 174bp cDNA clone
H0156344
H0156344.1 GI:29293403
EST
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; eudicotyledons I; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago.
1 (bases 1 to 273)
FORCES JORCE, J., Scott, A.D., Harris, A.R., Gonzalez, R.A., Bell, G.D., Torres, J.R., Imm, J.T., Weller, W. and May, G.D.
Medicago truncatula cDNA library from the Samuel Roberts Noble Foundation
Unpublished (2001)
Contact: May, G.D.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401, USA
Tel: 580 221 7491
Fax: 580 221 7490
Email: gdmay@noble.org

TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/2444 Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63109, USA
TEL: 314 286 1800
FAX: 314 286 1810
Email: est@wustl.edu

FEATURES
SOURCE
1..287
/organism="Medicago truncatula"
/db_xref="taxon:4880"
/clone="NF091H021R"
/tissue_type="seedlings"
/dev_stage="seedling"
/notes="Vector: Lambda ZAP. Specimens were prepared either by 100 Gy gamma or 0.5, 1, 5, or 10 kGy UV irradiation. Gamma-irradiated samples were harvested at 4, 12, 24 and 48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. RNA was prepared from poly(A⁺) enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directly ligated into the Uni-ZAP-XR vector (Stratagene) and packaged using the Gigapack III packaging extracts. Plasmids containing cDNA inserts were purified and excised from the recombinant DNA ZAP-XR vector using Fastap (PharMingen) and the PstI-XbaI strain XL1-Blue MRF⁺ (Stratagene). Excised plasmids were plated using SOB+ cells."

QUERY MATCH
Best local similarity 100.0% Ident. No. 0
Matches 26 Overlapped 0 Mismatches 0 Indels 0 Gaps 0

Y 176 ATCTCTTAAAAA
|||||
DB 248 ATCTCTTAAAAA
|||||

BASE COUNT
96 a 39 c 56 g 41 t 1 others

ORIGIN
1..693 Score 26 DB 14 Length 271
Best local similarity 100.0% Ident. No. 0
Matches 26 Overlapped 0 Mismatches 0 Indels 0 Gaps 0

Y 176 ATCTCTTAAAAA
|||||
DB 248 ATCTCTTAAAAA
|||||

RESULT 12
H0157100
CORGUS
DEFINITION
NF091H021R1094 174bp cDNA clone
H0157100
H0157100.1 GI:12690764
EST
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; eudicotyledons I; Fabales; Fabaceae; Papilionoideae; Phaseolales; Glycyne.
1 (bases 1 to 287)
SHOEMAKER, R., Keim, P., Vanden, L., Hoffmann, L., Gervais, V., Khanna, A., Bolla, J., Marita, M., Miller, M., Kowalski, M., Martin, J., Borek, C., Wille, T., Underwood, K., Stepien, M., Peterson, J., Allen, M., Borek, Y., Peterson, R., Sallier, T., Gilman, M., Pope, D., Harvey, N., Schaefer, E., Lister, E., Fahn, D., Gilman, J., Larsson, J., Cardenas, M., McCann, R., Watters, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63109, USA
TEL: 314 286 1800
FAX: 314 286 1810
Email: est@wustl.edu

FEATURES
SOURCE
1..287
/organism="Medicago truncatula"
/db_xref="taxon:4880"
/clone="NF091H021R"
/tissue_type="seedlings"
/dev_stage="seedling"
/notes="Vector: Lambda ZAP. Specimens were prepared either by 100 Gy gamma or 0.5, 1, 5, or 10 kGy UV irradiation. Gamma-irradiated samples were harvested at 4, 12, 24 and 48 hours after treatment. UV-irradiated samples were harvested 24 hours post-treatment. RNA was prepared from poly(A⁺) enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directly ligated into the Uni-ZAP-XR vector (Stratagene) and packaged using the Gigapack III packaging extracts. Plasmids containing cDNA inserts were purified and excised from the recombinant DNA ZAP-XR vector using Fastap (PharMingen) and the PstI-XbaI strain XL1-Blue MRF⁺ (Stratagene). Excised plasmids were plated using SOB+ cells."

ORGANISM

Danto perlo
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.

REFERENCES

Clarr, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marini, M., Eddy, S., Hillier, L., Kucaba, T., Martin, L., Beck, C., Wylie, T., Underwood, K., Steptoe, K., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Piro, J., Murray, N., Schork, F., Elter, F., Kohn, S., Shu, T., Jackson, Y., Cardenas, M., McEam, R., Waterston, R. and Wilson, R.

TITLE
JOURNAL
COMMENT

Wasn't Zehra'tish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel.: 314 286 1800
Fax: 314 286 1810
Email: zhratish@wason.wustl.edu
The library was constructed by Dr. Z. Goad, DNA Sequencing by:
Washington University Genome Sequencing Center St. Louis, Please
contact Zhiyuan Goad for further information on this library
(National University of Singapore, Department of Biological
Sciences, Lower Kent Ridge Road, Singapore 119250).
Seq primer: 73 bp from Amsterdam

FEATURES

source

1. 322
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="515712"
/clone_1lb "Ggtc zebrafish oocyte"
/sex="female"
/dev_stage="4-5 month"
/lab_host="DH10B (phage-resistant)"
/vector="pGm1.1 (see text). Vector: pBluescript SK⁺
Site 1: XhoI; Site 2: SbfI; Poly A: RNA was isolated from
the ovaries of 2 female adult zebrafish (4-5 month old).
cDNAs were made using oligo-dT primers and inserted into
lambda ZAP II vector (Stratagene) by Dr. T. Gong, in vitro
mass excised to plasmid SK⁺ following the Washington
University protocol
(http://genome.wustl.edu/esi/lambda_protocol.shtml).
Please contact Zhiyuan Gong for further information on
this library (National University of Singapore,
Department of Biological Sciences, Lower Kent Ridge Road,
Singapore 119260)."

116 a 48 c 59 q 99 t

Query Match

```

Query Match      1.68; Score 26; DB 13; Length 322;
Best Local Similarity 100.0%; Prcd. No. 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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177 FCTPCTAAAAAAAAAAAAA 202
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1b 291 TTCTGTAAAAAATAAAAC 316

Search completed: November 8, 2002, 06:06:02
Job time : 3076.49 secs

10 955 AATCAATTAATTAATTAATTAAT 940

RESULT 4

US-09-755-633-19
Sequence 12, Application US/09/46715
Patent No. 5544410

GENERAL INFORMATION:

APPLICANT: Tjian, Robert
APPLICANT: Comati, Lucio
APPLICANT: Dynlacht, Brian D.
APPLICANT: Hooey, Timothy
APPLICANT: Ruppert, Steffened
APPLICANT: Janosey, Naoko
APPLICANT: Wany, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: DATA BINDING PROTEIN ASSOCIATED FACTORS,
METHODS AND REAGENTS FOR THE SAME
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSER: FLHR, HOLBACH, TEST, ALBERTSON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy disk
COMPILED: IBM PC compatible
OPERATING SYSTEM: PC DOS 6.0
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09-755-633-19
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
AUTORUN/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE NUMBER: R-36627
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
FAX: 910 272299
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 972..3002
US-08-188-582-12

US-08-188-582-12

Query Match: 1.4% Score 24; DB 1; Length 3182;

Best Local Similarity: 100.0%; Prod. No. 0.46;

Matches: 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 TCTGTATAAAAAAAAAAAAAA 201
DB 40 TCTGTATAAAAAAAAAAAAAA 7

RESULT 4

US-09-755-633-19
Sequence 12, Application US/09/46715
Patent No. 5544410

GENERAL INFORMATION:

APPLICANT: Tjian, Robert
APPLICANT: Comati, Lucio
APPLICANT: Dynlacht, Brian D.
APPLICANT: Hooey, Timothy

APPLICANT: Ruppert, Steffened

APPLICANT: Janosey, Naoko

APPLICANT: Wany, Edith

APPLICANT: Weinzierl, Robert O.J.

TITLE OF INVENTION: DATA BINDING PROTEIN ASSOCIATED FACTORS,
METHODS AND REAGENTS FOR THE SAME

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSER: FLHR, HOLBACH, TEST, ALBERTSON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-4187

COMPUTER READABLE FORM:

COMPILED: IBM PC compatible

OPERATING SYSTEM: PC DOS 6.0

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 28-JAN-1994

CLASSIFICATION: 435

APPLICATION NUMBER: US-09-755-633-19

APPLICATION NUMBER: 36,627

REFERENCE NUMBER: R-36627

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

FAX: 910 272299

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 3182 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 972..3002

US-08-188-582-12

Query Match: 1.4% Score 24; DB 1; Length 3182;

Best Local Similarity: 100.0%; Prod. No. 0.46;

Matches: 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 TCTGTATAAAAAAAAAAAAAA 201
DB 30 TCTGTATAAAAAAAAAAAAAA 7

US-09-755-633-19

Sequence 12, Application US/09/46715

Patent No. 5544410

GENERAL INFORMATION:

APPLICANT: Tjian, Robert
APPLICANT: Comati, Lucio
APPLICANT: Dynlacht, Brian D.
APPLICANT: Hooey, Timothy

TITLE OF INVENTION: DATA BINDING PROTEIN ASSOCIATED FACTORS,
METHODS AND REAGENTS FOR THE SAME

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSER: FLHR, HOLBACH, TEST, ALBERTSON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-4187

COMPUTER READABLE FORM:

COMPILED: IBM PC compatible

OPERATING SYSTEM: PC DOS 6.0

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 28-JAN-1994

CLASSIFICATION: 435

APPLICATION NUMBER: US-09-755-633-19

APPLICATION NUMBER: 36,627

REFERENCE NUMBER: R-36627

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

FAX: 910 272299

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 3182 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 972..3002

US-08-188-582-12

Query Match: 1.4% Score 24; DB 1; Length 3182;

Best Local Similarity: 100.0%; Prod. No. 0.46;

Matches: 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 TCTGTATAAAAAAAAAAAAAA 201

DB 30 TCTGTATAAAAAAAAAAAAAA 7

FEATURE:
OTHER INFORMATION: Description of Additional Sequences: Patent Ref
OTHER INFORMATION: R8699
US-09-755-290-11

Query Match 1.48; Score 23; DB 4; Length 442;
Host Local Similarity 100.0%; Prod. No. 1.4;
Matches 23; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

UY 179 CTTGTAAGAAAAAAGAAAAA 201
DB 25 CTTGTAAGAAAAAAGAAAAA 3

RESULT 6
US-09-472-422A-35
Sequence: 6; Amino: 22; Length: 112A
Patent No. 641375
GENERAL INFORMATION:
APPLICANT: Rudolf Jung
APPLICANT: Francois Barthele
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
FILE REFERENCE: 0919
CURRENT APPLICATION NO: 09-08-11
CURRENT FILING DATE: 1999-08-11
PRIORITY APPLICATION NUMBER: US 62/099,692
PRIORITY FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO: 45
LENGTH: 442
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (2)...(257)
US-09-472-422A-35

Query Match 1.48; Score 23; DB 4; Length 442;
Host Local Similarity 100.0%; Prod. No. 1.4;
Matches 23; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

UY 179 CTTGTAAGAAAAAAGAAAAA 201
DB 404 CTTGTAAGAAAAAAGAAAAA 426

RESULT 7
US-08-849-751-1
Sequence 1; Application US/09849751
Patent No. 6190890
GENERAL INFORMATION:
APPLICANT: VAN DEN BROECK, HENRIETTE C.
APPLICANT: DE GRAAFF, HENDRIK H.
APPLICANT: VISSER, JACOB
APPLICANT: VAN OYEN, ALBERT J.J.
TITLE OF INVENTION: FORMAL CELLULOSES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Morrison & Pfeister
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
METHOD TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,751
FILING DATE: 12-JUN-1997

CLASSIFICATION: 4.5
PRIORITY APPLICATION: 61/755-633-19
APPLICATION NUMBER: 61/755-633-19
FILING DATE: 14-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Muroshige, Kato & B
REGISTRATION NUMBER: 45,054
FEDERAL REGISTER NUMBER: 45,054-2004-06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0308
TELEX:
INFORMATION FOR SEQ ID NO: 45
SEQUENCE CHARACTERISTICS:
LENGTH: 1017 base pairs
TYPE: nucleic acid
CHARACTERISTICS: Good
MOLECULE TYPE: DNA
HYDROLYTIC: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Aspergillus fumigatus
STRAIN: M400
INDIVIDUAL ISOLATE: Yes
FEATURE:
NAME/KEY: Coding sequence
LOCATION: 57...751
OTHER INFORMATION: Protein "Cellulase"

US-08-849-751-1
Query Match 1.48; Score 23; DB 4; Length 442;
Host Local Similarity 100.0%; Prod. No. 1.4;
Matches 23; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

UY 179 CTTGTAAGAAAAAAGAAAAA 201
DB 988 CTTGTAAGAAAAAAGAAAAA 100

RESULT 8
US-09-478-816-1
Sequence 1; Application US/09849751
Patent No. 6306635
GENERAL INFORMATION:
APPLICANT: VAN DEN BROECK, HENRIETTE C.
APPLICANT: DE GRAAFF, HENDRIK H.
APPLICANT: VISSER, JACOB
APPLICANT: VAN OYEN, ALBERT J.J.
TITLE OF INVENTION: FORMAL CELLULOSES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Morrison & Pfeister
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
METHOD TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/478,816
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION: 61/755-633-19
APPLICATION NUMBER: 61/755-633-19
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 61/755-633-19
FILING DATE: 14-JUN-1997
ATTORNEY/AGENT INFORMATION:

[illegible][illegible]

ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: PCD-38-M10
US-08-658-146-1

Query Match: 1.4%; Score 24; DB 1; Length 31571;
Best Local Similarity: 100.0%; Pred. No. 0.94;
Matches: 24; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

09 183 TAAAAAAAAAAAAAAAAAGG 205
DB 9172 TAAAAAAAAAAAAAAAAAGG 9194

RESULT 11
US-08-658-146-2

Sequence 2, Application US/08/658146
Patent No. 6071717

GENERAL INFORMATION:

APPLICANT: KLINGER, KATHERINE W

APPLICANT: LADNER, GREGORY M

APPLICANT: BORN, TIMOTHY D

APPLICANT: CONNORS, TIMOTHY D

APPLICANT: LACE, WILLIAM

APPLICANT: GERMING, GREGORY

APPLICANT: QIAN, PENG

TITLE OF INVENTION: POLYCYCLO PENTYL LIGAND

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESS: ONE MOUNTAIN ROAD

CITY: FRAMINGHAM

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 01701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/658,146

FILING DATE:

CLASSIFICATION: 435

AUTHOR/INVENTOR INFORMATION:

NAME: LASSIN, ELIZABETH

REGISTRATION NUMBER: 31,845

REFERENCE: PCT NUMBER, 0334-17.8

TELEPHONE: 508-872-8400

TELEFAX: 508-872-5415

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 5256 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-658-146-2

Query Match: 1.4%; Score 24; DB 3; Length 53526;
Best Local Similarity: 100.0%; Pred. No. 0.95;
Matches: 24; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

09 183 TAAAAAAAAAAAAAAAAAGG 205
DB 10157 TAAAAAAAAAAAAAAAAAGG 10179

RESULT 12
US-08-658-146-1
Sequence 1, Application US/08/658146

Patent No. 6071717

GENERAL INFORMATION:

APPLICANT: KLINGER, KATHERINE W

APPLICANT: LADNER, GREGORY M

APPLICANT: BORN, TIMOTHY D

APPLICANT: CONNORS, TIMOTHY D

APPLICANT: LACE, WILLIAM

APPLICANT: GERMING, GREGORY

APPLICANT: QIAN, PENG

TITLE OF INVENTION: POLYCYCLO PENTYL LIGAND

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESS: ONE MOUNTAIN ROAD

CITY: FRAMINGHAM

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 01701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/658,146

FILING DATE:

CLASSIFICATION: 435

AUTHOR/INVENTOR INFORMATION:

NAME: LASSIN, ELIZABETH

REGISTRATION NUMBER: 31,845

REFERENCE: PCT NUMBER, 0334-17.8

TELEPHONE: 508-872-8400

TELEFAX: 508-872-5415

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5357 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-658-146-1

Query Match: 1.4%; Score 24; DB 4; Length 53577;
Best Local Similarity: 100.0%; Pred. No. 0.95;
Matches: 24; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

09 183 TAAAAAAAAAAAAAAAAAGG 205
DB 10156 TAAAAAAAAAAAAAAAAAGG 10178

RESULT 13
US-08-658-146-1

Sequence 1, Application US/08/658146

Patent No. 6071717

GENERAL INFORMATION:

APPLICANT: KLINGER, KATHERINE W

APPLICANT: LADNER, GREGORY M

APPLICANT: BORN, TIMOTHY D

APPLICANT: CONNORS, TIMOTHY D

APPLICANT: LACE, WILLIAM

APPLICANT: GERMING, GREGORY

APPLICANT: QIAN, PENG

TITLE OF INVENTION: POLYCYCLO PENTYL LIGAND

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESS: ONE MOUNTAIN ROAD

CITY: FRAMINGHAM

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 01701

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB storage

COMPUTER: IBM compatible

```

1 OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
2 SOFTWARE: WordPerfect (Version 5.1)
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/08/44,503
5 FILING DATE: 04-MAY-1995
6 CLASSIFICATION: 4A5
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: US 08/008,895
9 FILING DATE: 19-JAN-1994
10 APPLICATION NUMBER: 07/949,849
11 FILING DATE: December 7, 1992
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Kurland, Richard J.
14 REGISTRATION NUMBER: 32,327
15 REFERENCE TO OTHER APPLICATIONS:
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: (213) 489-1600
18 TELEFAX: (213) 955-0440
19 TELETYPE: 67-4510
20 INFORMATION FOR SEQ ID NO: 41:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 27
23 TYPE: nucleic acid
24 STRANDEDNESS: single
25 TOPOLOGY: linear
26 US-08-44-503-41

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Query Match 1.3% Score 22; BB 1; Length 27;
Best Local Similarity 100.0%; Prod. No. 4.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
UY 1595 CTAAGAGCTAGCAAACTTAAAT 1616
DB 22 CTAAGAGCTAGCAAACTTAAAT 1

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```

RESULT 14
US-09-406-290 16/2
1 Sequence 16, Application us-09-406-290
2 Patent No. 6,221,645
3 GENERAL INFORMATION:
4 APPLICANT: Rovera, Giovanni
5 APPLICANT: Makhopadhyay, Sunil
6 TITLE OF INVENTION: METHODS FOR SOLID-PHASE AMPLIFICATION OF DNA TEMPLATE
7 FILE REFERENCE: 09924-10
8 CURRENT APPLICATION NUMBER: 09/070,629
9 CURRENT FILING DATE: 1999-05-06
10 NUMBER OF SEQ ID NOS: 43
11 SOFTWARE: PatentIn Ver. 2.0
12 SEQ ID NO: 16
13 TYPE: DNA
14 LENGTH: 40
15 ORGANISM: Artificial Sequence
16 FEATURE:
17 OTHER INFORMATION: Description of Artificial Sequence: Primer3
18 OTHER INFORMATION: KR713
19 US-09-406-290-16

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Query Match 1.3% Score 22; BB 4; Length 40;
Best Local Similarity 100.0%; Prod. No. 4.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
UY 180 TGTGAAAAAAAAAAAAAAAAAAAAA 201
DB 24 TGTGAAAAAAAAAAAAAAAAAAAAA 4

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RESULT 15
US-08-466-852-2
1 Sequence 2, Application US/08466852
2 Patent No. 5,681,946
3 GENERAL INFORMATION:

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1 APPLICANT:
2 TITLE OF INVENTION: A SINGLE STEP PURIFICATION METHOD
3 TITLE OF INVENTION: THE BROWN BROWN INTERFERON
4 NUMBER OF SEQUENCES: 1
5 CORRESPONDENT'S ADDRESS:
6 ADDRESSEE: Motek S. Brown
7 STREET: 126 East 110th St. Avenue
8 CITY: Railway
9 STATE: New Jersey
10 COUNTRY: USA
11 ZIP: 07065 0907
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Diskette, 5 1/4 in, 1.44k
14 COMPUTER: Apple Macintosh
15 ADDRESSING METHOD: System 7.0.1
16 SOFTWARE: Microsoft Word 6.0
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: 08/070,629
19 FILING DATE:
20 CLASSIFICATION: 4A4
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Patzelt, Gustav
23 REGISTRATION NUMBER: 33,333
24 REFERENCE TO OTHER APPLICATIONS:
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (908) 594 4777
27 TELEFAX: (908) 594 4777
28 INFORMATION FOR SEQ ID NO: 42:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 47 bases
31 TYPE: nucleic acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34 MOLECULE TYPE: DNA (mRNA)
35 US-08-466-852-2

```

```

Query Match 1.3% Score 22; BB 1; Length 47;
Best Local Similarity 100.0%; Prod. No. 4.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
UY 1595 CTAAGAGCTAGCAAACTTAAAT 1616
DB 8 CTAAGAGCTAGCAAACTTAAAT 4

```

Search completed: November 8, 2002 at 15:17
Job time: 151.514 sec



allergies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used to detect and in drug targeting.

Sequence 445 bp; 120 A; 68 C; 78 G; 79 T; 0 other.

Query Match: 7.8%; Score 129; Bp 21; Length 345;

Best Local Similarity: 100.0%; Prot. No. 1,36-372; Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

255 TTTTGGCGCTATGCTCTTTATTAAGACAGATTGGATTCATTATCGACAGC 314
|||||
249 TTTTGGCGCTATGCTCTTTATTAAGACAGATTGGATTCATTATCGACAGC 190
|||||
415 GTGGCTGAGGAGATTGATTTCAATGCTATATCCGAAACCTTTTAAACCA 374
|||||
189 GTGGCTGAGGAGATTGATTTCAATGCTATATCCGAAACCTTTTAAACCA 130
|||||
375 CAGTGGTG 384
|||||
129 CAGTGGTG 121

RESULT 8

AAZ5551

10 AAZ5551 standard; cDNA: 445 bp.

XX AAZ5551:

14-MAR-2000 (first entry)

Canine mature Interleukin-5 (IL-5) cDNA complement.

Interleukin-5 (IL-5) antibody: canine; immune response; immunoregulation; tumour; cancer; autoimmune disease; ss.

Canis familiaris.

W9961618-A2.

02-DEC-1999.

28-MAY-1999; 9900-0511942.

29-MAY-1998; 9905-0087305.

(HEK-) HESKA CODE.

Sim G., Yara S., Steele M., Wandeling R.

WP1: 2000-07262705.

P-PSDB; AAF58220.

Nucleic acids encoding immunoregulatory proteins from cats or dogs, useful for treating or preventing cat, tumours or autoimmune disease.

Claim 1b; Page 228; 264pp; English.

Sequences AAZ5551, 25551 represent cDNA sequences encoding canine interleukin-5 (IL-5). The invention relates to canine IL-5, canine or feline IL-5 ligand, canine or feline CD40, canine or feline CD134 (CD40 ligand), canine IL-5, canine IL-13, feline interleukin-alpha (IFN-alpha) and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleic acids which encode these immunoregulatory proteins. The proteins, their associated nucleic acids, specific antibodies and inhibitors may be used as vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans).

They may be used to treat autoimmune or infectious allergies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used to detect and in drug targeting.

Sequence 445 bp; 79 A; 76 C; 66 G; 120 T; 0 other.

Query Match:

Best Local Similarity: 100.0%; Prot. No. 1,36-372; Matches 129; Conservative 0; Mismatches 0;

255 TTTTGGCGCTATGCTCTTTATTAAGACAGATTGGATTCATTATCGACAGC 314
|||||
47 TTTTGGCGCTATGCTCTTTATTAAGACAGATTGGATTCATTATCGACAGC 190
|||||
315 GTGGCTGAGGAGATTGATTTCAATGCTATATCCGAAACCTTTTAAACCA 374
|||||
157 GTGGCTGAGGAGATTGATTTCAATGCTATATCCGAAACCTTTTAAACCA 130
|||||
375 CAGTGGTG 384
|||||
217 CAGTGGTG 225

RESULT 9

AAF7406/c

10 AAF7406 standard; cDNA: 445 bp.

XX AAF7406:

04-MAY-2001 (first entry)

Canine Interleukin-5 (IL-5) antibody: canine; immune response; immunoregulation; tumour; cancer; autoimmune disease; ss.

Canis sp.

W020011049-A2.

15-FEB-2001.

09-AUG-2000; 2000W-07262705.

10-AUG-1999; 9905-0087305.

(IDEX) IDEXX LAB CN.

Quo H., Lawton R., M. Steele M., Wandeling R.

WP1: 2001-19154219.

Novel canine interleukin-5 (IL-5) antibody: canine; immune response; immunoregulation; tumour; cancer; autoimmune disease; ss.

Claim 1; Page 35; 49pp; English.

The present invention relates to a canine interleukin-5 (IL-5) antibody. This antibody can be used to treat allergic diseases, autoimmune diseases, cancer and inflammatory reactions in dogs. The protein version of the IL-5 coding sequence shown in the

Sequence 393 bp; 120 A; 68 C; 78 G; 79 T; 0 other.

Query Match: 7.8%; Score 129; Bp 21; Length 345;

Best Local Similarity: 100.0%; Prot. No. 1,36-372; Matches 129; Conservative 0; Mismatches 0;

255 TTTTGGCGCTATGCTCTTTATTAAGACAGATTGGATTCATTATCGACAGC 314
|||||
47 TTTTGGCGCTATGCTCTTTATTAAGACAGATTGGATTCATTATCGACAGC 190
|||||
315 GTGGCTGAGGAGATTGATTTCAATGCTATATCCGAAACCTTTTAAACCA 374
|||||
157 GTGGCTGAGGAGATTGATTTCAATGCTATATCCGAAACCTTTTAAACCA 130
|||||
375 CAGTGGTG 384
|||||
217 CAGTGGTG 225

255 |||||GAGGCGTATGCTTTTATTAAGACAGCTTTGGAATATTTATTCACACAC 314
 204 TTTTTCATCTCTATGCTTTTATTAAGACAGCTTTGGAATATTTATTCACAC 345
 415 CTGAGGAGAGCTTTGCTTTTATTAAGCTATATTTGGAAGCTTTTATTTA 474
 144 CTGAGGAGAGCTTTGCTTTTATTAAGCTATATTTGGAAGCTTTTATTTA 85
 375 GAGTGGG 383
 84 CAGTGGG 76
 RESULT 10
 AAT50755/c
 10 AAT50755 standard, cDNA, 399 bp.
 AAT50755
 24-SEP-1997 (first entry)
 Ovine IL-5 cDNA.
 Ovine IL-5 cDNA.
 Cytokine ovine sheep interleukin-5; interleukin 12, IL-5, IL-12.
 Livestock, cow, stress, transport, vaccine adjuvant, veterinary
 cancer, immunosuppression, allergy, reproductive system, growth,
 early maturity, antibody, diagnosis, immunopotentiator,
 early bacterial endotoxin, bacterial endotoxin, gamma interferon, ss,
 secreted, 14M, 10A, bacterial endotoxin, gamma interferon, ss,
 Ovis aries aries.
 W09700321-AL.
 03-JAN-1997.
 14-JUN-1996: 96W0-AU00360.
 27-OCT-1995: 95AU-0006244.
 14-JUN-1995: 95AU-0003502.
 (GSP) J. COMMUNICATING SCI & IND RES OKG.
 Secow H, Wood P.
 WPI: 1997 07528/07.
 P-PSDB: AAW08479.
 Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
 adjuvants and to treat or prevent microbial infections in livestock
 (claim 6; page 41-42; 78pp; English).
 The sequences given in AAT50755 encode ovine interleukin-5 (IL-5),
 ovine IL-5 or IL-12 are used to treat and/or prevent infections in
 livestock (esp. cows and sheep). Particularly where the animals are
 stressed, e.g. during transport, IL-5 and IL-12 can also be used as
 adjuvants in vaccines for veterinary use (partic. weakly immunogenic
 subunit or synthetic peptide vaccines). They may also be used to
 treat cancer, immunosuppression and allergy. Is enhanced effect of the
 reproductive system and to promote growth or early maturity. Optionally
 interleukin can be delivered from constructs or delivery cells and
 antibodies are useful in ovine immunosystems for rapid diagnosis of
 infection. The interleukins are immunopotentiators, especially IL-5
 promotes growth of early haematopoietic precursor cells and generation
 of cytotoxic cells from lymphocytes, also it stimulates production and
 secretion of IgM and IgA (in synergism with bacterial endotoxin).
 IL-12 induces production of gamma-interferon by and proliferation
 of T and NK cells and increases the humoral specific cytotoxic
 lymphocyte response. The genetic constructs can also be used for
 in vitro production of IL-5 or -12.

Sequence 399 bp; 140 A; 77 C; 94 G; 99 T; 0 other;
 Query Match: 2.6%; (Score 43; 1P 18; Length 399;
 Best Local Similarity 100.0%; Posed No. 2; No-06)
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1517 GTCAGACAGCTTTGCTTTTATTAAGCTATATTTGGAAGCTTTTATTTA 1579
 110 GTCAGACAGCTTTGCTTTTATTAAGCTATATTTGGAAGCTTTTATTTA 68
 RESULT 11
 AAT50755/c
 10 AAT50755 standard; DNA; 520 bp.
 AAT50755
 24-SEP-1997 (first entry)
 Ovine IL-5 gene.
 Ovine IL-5 gene.
 Cytokine ovine sheep interleukin-5; interleukin 12, IL-5, IL-12.
 Livestock, cow, stress, transport, vaccine adjuvant, veterinary
 cancer, immunosuppression, allergy, reproductive system, growth,
 early maturity, antibody, diagnosis, immunopotentiator,
 early bacterial endotoxin, bacterial endotoxin, gamma interferon, ss,
 secreted, 14M, 10A, bacterial endotoxin, gamma interferon, ss,
 Ovis aries aries.
 W09700321-AL.
 03-JAN-1997.
 14-JUN-1996: 96W0-AU00360.
 27-OCT-1995: 95AU-0006244.
 14-JUN-1995: 95AU-0003502.
 (GSP) J. COMMUNICATING SCI & IND RES OKG.
 Secow H, Wood P.
 WPI: 1997 07528/07.
 P-PSDB: AAW08479.
 Nucleic acid encoding ovine interleukin-5 or -12 - used as vaccine
 adjuvants and to treat or prevent microbial infections in livestock
 (claim 6; page 39-40; 78pp; English).
 The sequences given in AAT50755 encode ovine interleukin-5 (IL-5),
 ovine IL-5 or IL-12 are used to treat and/or prevent infections in
 livestock (esp. cows and sheep). Particularly where the animals are
 stressed, e.g. during transport, IL-5 and IL-12 can also be used as
 adjuvants in vaccines for veterinary use (partic. weakly immunogenic

DB 44 ATTCTGTGTAACAAAAA 69

RESULT 14
AAH92592/

ID AAH92592 standard; DNA: 700 BP.

AC AAH92592:

DE 09-OCT-2001 (first entry)

DE Human inflammatory bowel disease related gene fragment 1281292a

XX Human inflammatory bowel disease; Crohn's disease; ulcerative colitis;

KM single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

XX chromosome 5q31-33; forensic test; gene therapy; ds.

OS Homo sapiens.

XX W0200142511-A2.

PN 14-JUN-2001.

XX 11-DEC-2000: 2000W0-0533430.

XX 10-DEC-1999: 990S-0170257.

XX 10-APR-2000: 2000W0-0196046.

XX (WHEED) WHITEHEAD INST BIOMEDICAL RES.

XX (ELI1-) ELIIPSIS BIOTHEAPARTICE 009P.

XX Daily M. Henson T.L. Lander E.E. Snow J. Zinkovitch K.

XX WPI: 2001 257874/78.

XX Testing for the presence of polymorphisms associated with inflammatory

XX bowel disease, using a hybridization assay

XX Disclosure: Page 261-262; 463pp; English.

XX The present invention describes a method for detecting the presence of

XX polymorphisms associated with inflammatory bowel diseases such as

XX ulcerative colitis and Crohn's disease. The methods can be used to detect

XX the presence of polymorphisms associated with inflammatory bowel

XX disease and correlating their occurrence with disease status. They may be

XX used in this way for phenotypic correlations; prognosis; paternity

XX testing, medicine and genetic analysis. The present sequence is a gene

XX containing a polymorphic site described in the exemplification of the

XX invention.

XX Sequence 700 BP: 216 A; 101 C; 125 G; 258 T; 0 other;

XX Query Match 1.6%; Score 26; DB 22; Length 700;

XX Best Local Similarity 100.0%; Pred. No. 3.4;

XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1234 AATGTAATTAATTAATTAATTTTAT 1259

DB 208 AATGTAATTAATTAATTAATTTTAT 183

KW plant pathogen; transgenic; disease resistance; corn; Nph1; ss.

OS Zea mays.

XX Key Location/Qualifiers

XX CDS 261..1491

XX /tag= a

XX W0200070069-A1.

XX 23-NOV-2000.

XX 12-MAY-2000: 2000W0-US13307.

XX 13-MAY-1999: 990S-0133965.

XX (MONS) MONSANTO CO.

XX Boudri OV, Rommens CMT, Srivastava N, Swords KM;

XX WPI: 2001 31511/02.

XX P-PSDB: AAH48093.

XX New acquired resistance genes Nph1 (from rice, *Oryza sativa*), and Nph2-1

XX and Nph2-2 from wheat, *Triticum aestivum*, useful for producing

XX transgenic plants with increased disease resistance

XX Example 1, Page 30; 101pp; English.

XX The invention relates to acquired resistance genes Nph1 from rice, and

XX Nph2-1 and Nph2-2 from wheat. The Nph1 and Nph2 polypeptides can be

XX expressed by standard recombinant methodology. The Nph1 and Nph2

XX polynucleotides or polypeptides can be used to obtain acquired

XX resistance in plants (e.g. wheat or rice) to control plant pathogens e.g.

XX the genes can be introduced to make transgenic plants with increased

XX disease resistance. The polynucleotides are also useful to produce probes

XX and primers used to detect the polynucleotides (to identify transgenic

XX plants containing an acquired resistance gene) and to isolate similar

XX sequences e.g. from other species. The polypeptides can be used to make

XX antibodies useful to monitor protein production e.g. in transgenic

XX plants. The present sequence represents a corn clone CP951 fl. cDNA

XX sequence, used in the identification of acquired resistance genes from

XX rice and wheat.

XX Sequence 2235 BP: 630 A; 452 C; 545 G; 573 T; 0 other;

XX Query Match 1.6%; Score 26; DB 22; Length 2235;

XX Best Local Similarity 100.0%; Pred. No. 2.8;

XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 176 ATTCTGTGTAACAAAAA 201

DB 2171 ATTCTGTGTAACAAAAA 2196

Search completed: November 7, 2002, 22:02:57

Job time : 450.508 secs


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LOCUS      AX083939/c          407 bp     DNA           linear       01 DEC 94   JAL 22-UN-E601
DEFINITION Sequence 1 from Patent WO0110149.
ACCESSION  AX083939
VERSION    AX083939.2   GI:14532940
SOURCE     dog.
ORGANISM   Canis familiaris
            Eukaryota; Metazoa; Chordata; Cinelata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE  1 (bases 1 to 405)
AUTHORS   Guo,H., Lawton,R., Mermer,B. and Aiyappa,A.P.
TITLE      Methods and compositions concerning canine Interleukin 5
PDBLINK   PDB: 0111049-A 1 15-FEB-2001:
JOURNAL    IDEXX LABORATORIES, INC. (US)
COMMENT    On Jun 24, 2001 this sequence version replaced gi:13185501.
FEATURES             location/qualifiers
     source          1..405
                    /organism="Canis familiaris"
                    /db_xref="taxon:9615"
BASE COUNT      131 a      77 c      94 g      103 t
ORIGIN
query Match              8.4%; Score 139; DB 6; Length 405;
Best Local Similarity 100.0%; Prod. No. 6_9e-59;
Matches 139, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
DY      140G  CGCATCGTATAGCAAAATTGCATGATGTGGATGAAGAAGTAAGAGTCCTCCATCTAT 154R
DB      144  CCAATGCCATATGAGCAAAATTTGCATGATGTGGATGAAGAAGTAAGAGTCCTCCATCTAT 154R
DY      154G  TGTATGATGGCATTCTTGTCAGCAAGCAAGCACAGAACATATAGAGAGAGAGTAGCAAA 160R
DB      84    TGTATGATGGCATTCTTGTCAGCAAGCAAGCACAGAACATATAGAGAGAGAGTAGCAAA 25
DY      160G  AGCCAATTCACAAGCAATT 162Z
DB      24    ACTCAATTCAGAGCAATT 6
RESULT 3
LOCUS      AF331919/c          610 bp     mRNA         linear       MAR 04-UCI-2000
DEFINITION Canis familiaris interleukin-5 mRNA, complete cds.
ACCESSION  AF331919
VERSION    AF331919.1   GI:15919180
KEYWORDS
SOURCE     .
ORGANISM   Canis familiaris
            Canis familiaris
            Eukaryota; Metazoa; Chordata; Cinelata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE  1 (bases 1 to 610)
AUTHORS   Yang,S., Seifried,K.S., Weber,E. and McGall,C.
TITLE      Canine interleukin-5: molecular characterization of the gene and
            expression of biologically active recombinant protein
JOURNAL    J. Interferon Cytokine Res. 21 (6), 361-367 (2001)
MEDLINE    21334408
PubMed     11440633
REFERENCE  2 (bases 1 to 610)
AUTHORS   Yang,S.
TITLE      Direct Submission
JOURNAL    Submitted (22-DEC-2000) Immunology, Hoeska Corporation, 1613
            Prospect Parkway, Ft Collins, CO 80525, USA
FEATURES             location/qualifiers
     source          1..610
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                    /db_xref="taxon:9615"
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                /product="Interleukin 5"
                /protein_id="AA110715.1"

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[illegible]

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ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Placentalia; Canidae; Canis.
REFERENCE
1 (bases 1 to 356)
German, A.J., Holps, C.R., Bartley, R., Hall, E.H., and Day, M.T.
Cloning and sequencing of canine Interleukin-5.
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 356)
German, A.J., Holps, C.R., Bartley, R., Hall, E.H., and Day, M.T.
Direct Submission
Submitted (12-SEP-1998) to EMBL, GenBank, and DDBJ/NCBI
University of Bristol, Langford House, Langford, Bristol, North
Somerset BS40 5DU, United Kingdom
Location/Qualifiers
Locus: IL-5
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/db_xref="taxon:9615"
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/contig_start=1
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/contig_size=356
/contig_name="Canis familiaris IL-5"
/contig_accession="AF044963.1"
/contig_version="1"
/contig_date="1998-09-04"
/contig_source="Novartis Institutes for Biomedical Research,
NIDDK, Chevy Chase, MD, USA; NIH, NIDDK, NIH, Bethesda, MD,
USA; NIDDK, NIH, Bethesda, MD, USA"
BASE COUNT
120 a 70 c 77 g 89 t
ORIGIN
Query Match 7.8% Score 129.00 41: length 356:
Best local similarity 100.0%: Prod. No. 8,10-54:
Matches 129: conservative 0: Mismatches 0: Indels 0: Gaps 0.

UY 255 TTTTGGAGGCTAGCTGCTTTTATTTAAACAACTTTTCAGATCTTATTCACAGC 314
|||||
DB 270 TTTTGGAGGCTAGCTGCTTTTATTTAAACAACTTTTCAGATCTTATTCACAGC 211
|||||
UY 415 GTCCGCTGAGGAGTTTGGTCTTCAAGTGTATACCTTAAAGATCTTTAAAGCA 374
|||||
DB 210 CTTCCAGGAGGAGTTTGGTCTTCAAGTGTATACCTTAAAGATCTTTAAAGCA 151
|||||
UY 675 GAGTGGGAG 483
|||||
DB 150 GAGTGGGAG 142
|||||

RESULT 6
CA035048/c
LOCUS
DEFINITION
Ovis aries Interleukin-5 mRNA, complete cds.
ACCESSION
U35048
VERSION
U35048.1 GI:4096663
KEYWORDS
Ovis aries.
SOURCE
Ovis aries.
Organism
Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE
1 (bases 1 to 520)
Snow, H.C., David, M., Liu, M., Watson, P.D., Hirst, J., and Wood, P.R.
Cloning of ovine Interleukin-5 cDNA
Unpublished (1995)
REFERENCE
2 (bases 1 to 520)
Snow, H.C.
Direct Submission
Submitted (30-AUG-1995) to EMBL, GenBank, and DDBJ/NCBI
Corner of Flemington Rd and Park Drive, Melbourne, Vic 3052,
Australia
Location/Qualifiers
Locus: IL-5
/organism="Ovis aries"
/db_xref="taxon:9940"
46..444
CDS

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/contig_start=1
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/contig_accession="AF044963.1"
/contig_version="1"
/contig_date="1998-09-04"
/contig_source="Novartis Institutes for Biomedical Research,
NIDDK, Chevy Chase, MD, USA; NIH, NIDDK, NIH, Bethesda, MD,
USA; NIDDK, NIH, Bethesda, MD, USA"
BASE COUNT
166 a 99 c 124 g 111 t
ORIGIN
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Best local similarity 100.0%: Prod. No. 2,70-10:
Matches 43: conservative 0: Mismatches 0: Indels 0: Gaps 0.

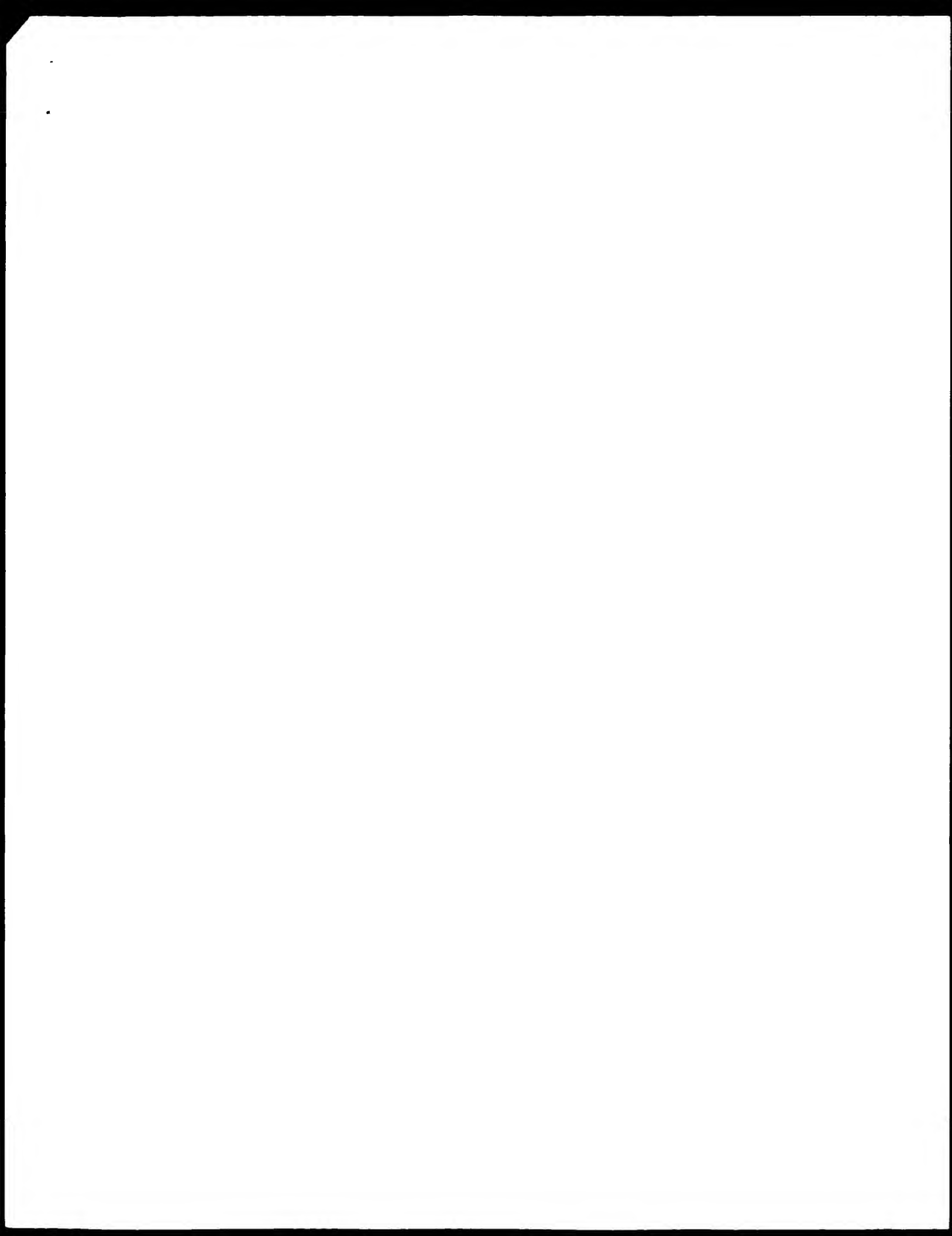
UY 1517 GTGACAGCATCTCAAGAGCTCTGAGGAGAGTATCATGATG 1559
|||||
DB 155 GTGACAGCATCTCAAGAGCTCTGAGGAGAGTATCATGATG 113
|||||

RESULT 7
CA035048/c
LOCUS
DEFINITION
Ovis aries Interleukin-5 (IL5) mRNA, partial.
ACCESSION
U37052
VERSION
U37052.1 J13897.08
KEYWORDS
Ovis aries.
SOURCE
Ovis aries.
Organism
Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE
1 (bases 1 to 1140)
Bryson, O.D., Viny, E., Burdon, M., and Boyd, A.W.
Structure of the sheep Interleukin-5 gene
Unpublished
REFERENCE
2 (bases 1 to 1140)
Bryson, O.D.
Direct Submission
Submitted (09-NOV-1994) to EMBL, GenBank, and DDBJ/NCBI
University of Melbourne, Flemington Rd., Parkville,
Victoria, 3052, Australia
Location/Qualifiers
Locus: IL5
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/contig_accession="AF044963.1"
/contig_version="1"
/contig_date="1998-09-04"
/contig_source="Novartis Institutes for Biomedical Research,
NIDDK, Chevy Chase, MD, USA; NIH, NIDDK, NIH, Bethesda, MD,
USA; NIDDK, NIH, Bethesda, MD, USA"
BASE COUNT
63 a 168 c 198 g 411 t
ORIGIN
Query Match 2.6% Score 43.00 41: length 1140:
Best local similarity 100.0%: Prod. No. 2,70-10:
Matches 43: conservative 0: Mismatches 0: Indels 0: Gaps 0.

UY 1517 GTGACAGCATCTCAAGAGCTCTGAGGAGAGTATCATGATG 1559
|||||
DB 679 GTGACAGCATCTCAAGAGCTCTGAGGAGAGTATCATGATG 547
|||||

RESULT 8
SSC010088/c
LOCUS
DEFINITION
Sus aerea mRNA for Interleukin-5.
ACCESSION
AF010088
405 bp. mRNA. Linear. MAX 03-FEB-2000

```

XX detection, and in drug targeting.

XX Sequence 445 bp; 79 A; 78 G; 68 G; 120 T; 0 other:

Query Match 56.68; Score 445; DB 21; Length 345;

Host Local Similarity 100.0%; Pred. No. 2,46; 1697

Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

UY 86 TTTCCTGTCATGAAATGCGATGATTAACGTGGGAGACAGCTTCACATCTGTCGCAT 145
    |||||||
DB 345 TTTCCTGTCATGAAATGCGATGATTAACGTGGGAGACAGCTTCACATCTGTCGCAT 286
    |||||||
UY 146 CATGAAATCTGGGATGATGAGGAACTGATGATGATGATGATGATGATGATGAT 205
    |||||||
DB 285 CATGAAATCTGGGATGATGAGGAACTGATGATGATGATGATGATGATGATGAT 226
    |||||||
UY 206 CATGAAATCTGGGATGATGAGGAACTGATGATGATGATGATGATGATGATGAT 265
    |||||||
DB 225 CATGAAATCTGGGATGATGAGGAACTGATGATGATGATGATGATGATGATGAT 166
    |||||||
UY 266 CATGAAATCTGGGATGATGAGGAACTGATGATGATGATGATGATGATGATGAT 325
    |||||||
DB 165 CATGAAATCTGGGATGATGAGGAACTGATGATGATGATGATGATGATGATGAT 106
    |||||||
UY 326 CATGAAATCTGGGATGATGAGGAACTGATGATGATGATGATGATGATGATGAT 485
    |||||||
DB 105 CATGAAATCTGGGATGATGAGGAACTGATGATGATGATGATGATGATGATGAT 46
    |||||||
UY 486 CATGAAATCTGGGATGATGAGGAACTGATGATGATGATGATGATGATGATGAT 490
    |||||||
DB 45 CATGAAATCTGGGATGATGAGGAACTGATGATGATGATGATGATGATGATGAT 1
    |||||||

```

RESULT 8

AA74306

DB AAF74306; standard; DNA; 343 bp;

XX AAF74306;

XX 04-MAY-2001 (first entry)

DE Canine interleukin-5 coding sequence #4.

XX Note: Interleukin-5 (IL-5) allergy: cancer gene therapy;

XX Inflammatory reaction; ds.

XX Canis sp.

XX W020011049-A2.

XX 15-FEB-2001.

XX 09-AUG-2000; 2000W-0821651.

XX 10-AUG-1999; 9908-0371615.

XX (IDEX-) IDEXX LAB INC.

XX Guo H., Lawton R., Mermer B., Alyappa AP;

XX WPI; 2001-191542/19

XX Novel canine interleukin 5 polypeptide and polypeptides are used for
 XX generating antibodies which are useful in treating allergies in dogs -
 XX Claim 1; Page 46; 48pp; English.

XX The present invention provides the protein and coding sequences of the
 XX canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
 XX cancer and inflammatory reactions in dogs. The present sequence is one
 XX version of the IL-5 coding sequence shown in the specification.

XX Sequence 443 bp; 128 A; 92 G; 86 G; 97 T; 0 other:

Query Match 44.3%; Score 278; DB 22; Length 493;

Host Local Similarity 100.0%; Pred. No. 2,46-140;

Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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UY 131 ACATGCTGCTGATTCATGTCGAACTGGGATGATGATGATGATGATGATGAT 190
    |||||||
DB 1 ACATGCTGCTGATTCATGTCGAACTGGGATGATGATGATGATGATGATGATGAT 60
    |||||||
UY 191 CCGTAAATATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 250
    |||||||
DB 61 CCGTAAATATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
    |||||||
UY 251 AAGAGCAAACTGCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 310
    |||||||
DB 121 AAGAGCAAACTGCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
    |||||||
UY 411 AAGAGCAAACTGCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 470
    |||||||
DB 181 AAGAGCAAACTGCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
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UY 471 TTCTAGACTAGCTGCAAGATTTCTTGGT 490
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DB 241 TTCTAGACTAGCTGCAAGATTTCTTGGT 270
    |||||||

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RESULT 9

AA74305

DB AAF74305; standard; DNA; 252 bp;

XX AAF74305;

XX 04-MAY-2001 (first entry)

DE Canine interleukin 5 coding sequence #2.

XX Note: Interleukin-5 (IL-5) allergy: cancer gene therapy;

XX Inflammatory reaction; ds.

XX Canis sp.

XX W020011049-A2.

XX 15-FEB-2001.

XX 09-AUG-2000; 2000W-0821651.

XX 10-AUG-1999; 9908-0371615.

XX (IDEX-) IDEXX LAB INC.

XX Guo H., Lawton R., Mermer B., Alyappa AP;

XX WPI; 2001-191542/19.

XX P-PSDB; AAF72616.

XX Novel canine interleukin 5 polypeptide and polypeptides are used for
 XX generating antibodies which are useful in treating allergies in dogs -
 XX Example 1; Fig 1; 48pp; English.

XX The present invention provides the protein and coding sequences of the
 XX canine interleukin 5 (IL-5) protein. This can be used to treat allergies,
 XX cancer and inflammatory reactions in dogs. The present sequence is one
 XX version of the IL-5 coding sequence shown in the specification.

XX Sequence 252 bp; 69 A; 54 G; 50 G; 69 T; 0 other:

Query Match 41.3%; Score 252; DB 22; Length 252;

Host Local Similarity 100.0%; Pred. No. 6,56-121;

Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 29 ATGAGAAATGCTGTCGAAATTCGATCTTCGATCTTCGATCTTCGATCTTCGATCT 88

Fri Nov 8 12:51:21 2002

us-09-755-633-4.rng

Page 10

Search completed: November 7, 2002, 22:02:40
Index time: 166.172 secs

PS Claim 24: Page 224: 264pp: English.

XX
 XX Sequences AAY58219-Y58220 represent encoded and mature
 CC canine interleukin-5 (IL-5). The invention relates to canine
 CC IL-4, canine or feline IL-3 ligand, canine or feline GM-CSF, canine or
 CC feline CD134 (CD140 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins, the proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat allergic or inflammatory diseases including
 CC allergies, tumors, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense
 CC oligonucleotides). The proteins may be used to raise antibodies for
 CC screening for modulators of activity, while the antibodies may be used in
 CC detection and in direct treatment.

SO Sequence 134 AA:

Query Match 100.0% Score 696; DB 21; Length 134;
 Best Local Similarity 100.0%; Evid. No. 1,40-75;
 Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

07 1 MELLINSLALAAVSAVAVIRMRKVAETLTLSHRTWLSGGCHHTPTERRKH 60
 10 IIRKILRSGALAAVSAVAVIRMRKVAETLTLSHRTWLSGGCHHTPTERRKH 60
 08
 09 61 VCTTTEVEVCTTTEVEVCTTTEVEVCTTTEVEVCTTTEVEVCTTTEVEV 120
 11 IIRKILRSGALAAVSAVAVIRMRKVAETLTLSHRTWLSGGCHHTPTERRKH 60
 12 61 CTCTTTEVEVCTTTEVEVCTTTEVEVCTTTEVEVCTTTEVEVCTTTEVEV 120
 07 121 VFLGVINTEWTPES 134
 10 IIRKILRSGALAAVSAVAVIRMRKVAETLTLSHRTWLSGGCHHTPTERRKH 60
 12 121 VFLGVINTEWTPES 134

RESULT 2
 AAY58215
 ID AAY58215 standard; Protein: 134 AA.
 XX
 AC AAY58215:
 XX
 DT 04 MAY-2001 (first entry)
 XX
 DE Canine interleukin 5 protein #1.
 XX
 KW [dog: Interleukin-5; IL-5; allergy; cancer; gene therapy;
 XX inflammatory reaction;
 XX
 OS Canis sp.
 XX
 FN W/200112049 AZ.
 XX
 PD 15 FEB-2001.
 XX
 PF 09-AUG-2000; 2000W0-0521651.
 XX
 PR 10 AUG-1999; 990S-0071615.
 XX
 PA (INDEX-) INDEX LAB INC.
 XX
 PI Guo H, Lawton R, Mormer B, Aliyappa AP;
 XX
 DR W/1: 2001-141542/19.
 DR N FISH: AAY5821500.
 XX
 PT Novel canine interleukin 5 polypeptide and polypeptides are used for
 PI generating antibodies which are useful in treating allergies in dogs.

XX
 PS Claim 24: Page 46-47; 44pp: English.

XX
 XX The present invention provides the protein and coding sequences of the
 CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
 CC cancer and inflammatory reactions in dogs. The present sequence is one
 CC version of the IL-5 protein shown in the specification.

SO Sequence 134 AA:

Query Match 98.7% Score 627; DB 22; Length 134;
 Best Local Similarity 99.1%; Evid. No. 1,40-74;
 Matches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

07 1 MELLINSLALAAVSAVAVIRMRKVAETLTLSHRTWLSGGCHHTPTERRKH 60
 10 IIRKILRSGALAAVSAVAVIRMRKVAETLTLSHRTWLSGGCHHTPTERRKH 60
 08
 09 61 VCTTTEVEVCTTTEVEVCTTTEVEVCTTTEVEVCTTTEVEVCTTTEVEV 120
 11 IIRKILRSGALAAVSAVAVIRMRKVAETLTLSHRTWLSGGCHHTPTERRKH 60
 12 61 CTCTTTEVEVCTTTEVEVCTTTEVEVCTTTEVEVCTTTEVEVCTTTEVEV 120
 07 121 VFLGVINTEWTPES 134
 10 IIRKILRSGALAAVSAVAVIRMRKVAETLTLSHRTWLSGGCHHTPTERRKH 60
 12 121 VFLGVINTEWTPES 134

RESULT 4
 AAY58220
 ID AAY58220 standard; Protein: 115 AA.
 XX
 AC AAY58220:
 XX
 DT 14 MAR-2000 (first entry)
 XX
 DE Canine mature interleukin-5 (IL-5).
 XX
 KW Interleukin 5; IL-5; antibody; canine; inhibitor; immune response;
 XX [immune regulation; tumor; cancer; autoimmune disease]; vaccine.
 XX
 OS Canis familiaris.
 XX
 FN W/9961618 AZ.
 XX
 PD 02 DEC-1999.
 XX
 PF 24 MAY-1999; 99W0-0511042.
 XX
 PR 29 MAY-1998; 98JS-0087406.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Elm G, Yana S, Dreitz M, Wiedertling RS;
 XX
 DR W/1: 2000-072624/06.
 DR R FISH: AAY55550, AAY55551.
 XX
 PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PI useful for treating or preventing e.g., tumors or autoimmune disease.

PS Claim 3b: Page 227; 264pp: English.

XX
 XX Sequences AAY58219-Y58220 represent encoded and mature
 CC canine interleukin-5 (IL-5). The invention relates to canine
 CC IL-4, canine or feline IL-3 ligand, canine or feline GM-CSF, canine or
 CC feline CD134 (CD140 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins, the proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including

[illegible][illegible]


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1b 1507 TTGATGATAGGCAATGGGTAATTTCTTTTATGCTGACAGCTTTTAAATGCTATGG 1448
G 212 GAAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 271
1b 1447 GAAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1388
G 272 TAAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 340
1b 1387 TAAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1328
G 331 TTAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 390
1b 1327 TTAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1268
G 391 TCGTGAATAAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 450
1b 1267 TCGTGAATAAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1208
G 451 TTAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 510
1b 1207 TTAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1148
G 511 TTAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 570
1b 1147 TTAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1088
G 571 GCTGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 630
1b 1087 GCTGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1028
G 631 GATGTCATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 690
1b 1027 GATGTCATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 969
G 691 GTCATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 750
1b 967 GTCATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 908
G 751 TTTGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 810
1b 907 TTTGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 848
G 811 AATATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 870
1b 847 AATATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 788
G 871 TAAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 930
1b 787 TAAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 728
G 931 ATGATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 990
1b 727 ATGATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 668
G 991 AGGATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1050
1b 667 AGGATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 608
G 1051 TCAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1110
1b 607 TCAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 548
G 1111 TTAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1170
1b 547 TTAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 488
G 1171 AGAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1230
1b 487 AGAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 429
G 1231 GATGTCATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1290
1b 428 GATGTCATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 369

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G 1291 AATGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1350
1b 308 AATGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1310
G 1351 GATGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1410
1b 308 GATGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1370
G 1411 TAAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1470
1b 219 TAAATATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1430
G 1471 TTTGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1530
1b 188 TTTGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1490
G 1531 TTTGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1590
1b 128 TTTGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1550
G 1591 AATGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1650
1b 68 AATGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1610
G 1651 TTTGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1710
1b 8 TTTGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1670

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RESULT 3

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US-09-755-633-21
1 Sequence 21, Affiliation: US-09-755-633
2 Patient No. US200201272-A
3 CURRENT INFORMATION:
4 APPLICANT: Yang, Shunlin
5 APPLICANT: Meng, Jia
6 APPLICANT: Meng, Jia
7 TITLE OF INVENTION: CARBON AND POLYMER MEMBRANE FOR
8 FILE REFERENCE: IN 2002/01
9 CURRENT AFFILIATION NUMBER: 2002/01
10 PRIOR FILING DATE: 2002/01/27
11 PRIOR APPLICATION NUMBER: 2002/01/27
12 PRIOR FILING DATE: 2002/01/27
13 PRIOR APPLICATION NUMBER: 2002/01/27
14 NUMBER OF SEQ ID NOS: 21
15 SOFTWARE: Patent In
16 SEQ ID No 21
17 LENGTH: 671
18 TYPE: DNA
19 ORGANISM: Cauda
20 US-09-755-633-21

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Query Match 24/24 Score 406 Db 167
Host Local Similarity 100% Fred No. 5/10/04
Matches 406 Conserved 0 Mismatches 0

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G 1 AGGTAATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1670
1b 1 AGGTAATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1630
G 1671 TTTGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1730
1b 61 TTTGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1690
G 1731 AGGTCATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1790
1b 121 AGGTCATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1750
G 1791 AGGTCATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1850
1b 121 AGGTCATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1810
G 1851 TTTGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1910
1b 181 TTTGATATAT AATGGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGT 1870

```


Patent No. US20020142981A1
 GENERAL INFORMATION:
 APPLICANT: Hottel, Daniel L.
 APPLICANT: Workley, Joseph G.
 APPLICANT: Schett, Owe
 APPLICANT: Gene Logic, Inc.
 TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
 FILE REFERENCE: 44921-5028-W0
 CURRENT APPLICATION NUMBER: US-09/7890,107
 CURRENT FILING DATE: 2001-06-14
 PRIOR APPLICATION NUMBER: US 60/211,479
 PRIOR FILING DATE: 2000-06-14
 PRIOR APPLICATION NUMBER: US 60/237,054
 PRIOR FILING DATE: 2000-10-02
 NUMBER OF SEQ ID NOS: 4950
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 1402
 LENGTH: 240
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: US-09-755-633-18.rnpb
 US-09-880-107-1302

Query Match: 1.44; Score: 23; DB: 10; Length: 240
 Best Local Similarity: 100.0%; Prod. No.: 6
 Matches: 23; Conservative: 0; Mismatches: 0; Gaps: 0
 Y: 1458 TTTTCTTTTCTTTTCTTTTACAG 1480
 TTTTCTTTTCTTTTCTTTTCTTTTCTTTT
 DB: 19 TTTTCTTTTCTTTTCTTTTACAG 41

RESULT 15
 US-09-917-800A-393
 Sequence 393, Application US-09/917800A
 Patent No. US2002019462A1
 GENERAL INFORMATION:
 APPLICANT: Mendrick, Donna
 APPLICANT: Porter, Mark
 APPLICANT: Johnson, Kory
 APPLICANT: Castle, Arthur
 APPLICANT: Elashoff, Michael
 APPLICANT: Gene Logic, Inc.
 TITLE OF INVENTION: Molecular Toxicology Modeling
 FILE REFERENCE: 44921-5038-US
 CURRENT APPLICATION NUMBER: US-09/917,800A
 CURRENT FILING DATE: 2001-07-31
 PRIOR APPLICATION NUMBER: US 60/222,040
 PRIOR FILING DATE: 2000-07-31
 PRIOR APPLICATION NUMBER: US 60/222,880
 PRIOR FILING DATE: 2000-11-02
 PRIOR APPLICATION NUMBER: US 60/293,829
 PRIOR FILING DATE: 2001-05-11
 PRIOR APPLICATION NUMBER: US 60/290,645
 PRIOR FILING DATE: 2001-05-15
 PRIOR APPLICATION NUMBER: US 60/292,336
 PRIOR FILING DATE: 2001-05-22
 PRIOR APPLICATION NUMBER: US 60/295,798
 PRIOR FILING DATE: 2001-06-06
 PRIOR APPLICATION NUMBER: US 60/297,457
 PRIOR FILING DATE: 2001-06-13
 PRIOR APPLICATION NUMBER: US 60/298,854
 PRIOR FILING DATE: 2001-06-19
 PRIOR APPLICATION NUMBER: US 60/303,459
 PRIOR FILING DATE: 2001-07-09
 NUMBER OF SEQ ID NOS: 1740
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 393
 LENGTH: 298
 TYPE: DNA
 ORGANISM: Rattus norvegicus
 FEATURE:

OTHER INFORMATION: Database Accession No. US20020142981A1
 US-09-917-800A-393
 Query Match: 1.44; Score: 23; DB: 10
 Best Local Similarity: 100.0%; Prod. No.: 6
 Matches: 23; Conservative: 0; Mismatches: 0
 Y: 1459 TTTTCTTTTCTTTTCTTTTACAG 1480
 TTTTCTTTTCTTTTCTTTTCTTTTCTTTT
 DB: 1 TTTTCTTTTCTTTTCTTTTACAG 41
 Match completed: November 8, 2002 11:10:17
 Job time: 98.139 secs



Genforce version 5.1.1
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OM protein - protein search, using SW model

Run on: November 8, 2002, 11:00:04 : Search time 2.6787 seconds

(without alignments)
544,034 Million cell updates/sec

Title: US-09-755-633-5

Perfect score: 696

Sequence: 1 MEMLINSLALGAAVSAF.....FLDYVLELV NLEWPEES 134

Scoring table: HDOSUM62

Gapop 10.0 : Gapext 0.5

Searched: 284224 seqs, 9514422 residues

Total number of hits satisfying chosen parameters: 284224

Minimum hit seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database: PIR 743*

1: p111**

2: p112**

3: p113**

4: p114**

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	591	79.2	134	2	J05116
2	486	61.8	134	1	A28477
3	476	54.0	134	1	ICM85
4	461	51.9	142	1	A48418
5	84.5	12.0	1199	2	G59698
6	78.5	11.3	258	2	147758
7	77.5	11.1	441	2	G84876
8	77	11.1	478	2	134745
9	74.5	10.7	1242	2	B59442
10	74.5	10.6	253	2	147757
11	72.5	10.4	207	2	G71914
12	72.5	10.4	151	2	G33816
13	72.5	10.4	649	2	G33813
14	72.5	10.4	679	2	G33811
15	72.5	10.4	686	2	G33815
16	72	10.3	253	2	G59698
17	72	10.3	401	2	G28653
18	71	10.2	216	2	B59498
19	71	10.2	400	2	P84594
20	71	10.2	428	2	P84187
21	71	10.2	446	2	S74228
22	71	10.2	461	2	134898
23	71	10.2	513	2	112932
24	70.5	10.1	1555	2	110432
25	70	10.1	215	2	P45955
26	70	10.1	943	2	A59250
27	70	10.1	1471	2	P64698
28	70	10.1	1535	2	134356
29	69.5	10.0	1188	2	G54889

40	59	9.9	547	2	G59698
41	59	9.9	447	2	S50006
42	59	9.9	447	2	S50006
43	59	9.9	447	2	S50006
44	59	9.9	447	2	S50006
45	59	9.9	447	2	S50006
46	59	9.9	447	2	S50006
47	59	9.9	447	2	S50006
48	59	9.9	447	2	S50006
49	59	9.9	447	2	S50006
50	59	9.9	447	2	S50006
51	59	9.9	447	2	S50006
52	59	9.9	447	2	S50006
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63	59	9.9	447	2	S50006
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69	59	9.9	447	2	S50006
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84	59	9.9	447	2	S50006
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94	59	9.9	447	2	S50006
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ALIGNMENTS

RESULT 1

J05116

Interleukin-5 precursor - bovine

CSpecies: Bos primigenius (adult) (adult)

CDate: 02-Feb-1997 #sequence version 27 Feb 1997 #1

CAccession: J05116

R:Mothers: B. Gobright: B. Stock: B. F.

Gene 176, 273-274, 1996

A>Title: The nucleotide sequence of the bovine interleukin-5 precursor cDNA

AReference number: J05116 (Mol Cell Biol 16:7544-7548, 1996)

A:Accession: J05116

A:Molecule type: mRNA

A:Residues: 1-134 - MEM

A:Cross-references: EMBL: J05116 (Mol Cell Biol 16:7544-7548, 1996)

A:Experimental source: lymphocytes

A:Comment: This protein belongs to the IL-5 family

C:Genetics:

A:Gene: IL-5

C:Superfamily: Interleukin-5

C:Keywords: cytokine, signal sequence, status predicted: SL

F1-19/Domain: signal sequence #status predicted: SL

F22-134/Domain: signal sequence #status predicted: SL

F63/Domain: signal sequence #status predicted: SL

F76-134/Domain: signal sequence #status predicted: SL

F107/Domain: signal sequence #status predicted: SL

F107/Domain: signal sequence #status predicted: SL

Query Match

Best local similarity: 79.981 Prod. No. 1 to 101

Matches: 107 Conserved: 107 Missmatches: 02

Q7 1 MEMLINSLALGAAVSAF.....FLDYVLELV NLEWPEES 134

Q7 1 MEMLINSLALGAAVSAF.....FLDYVLELV NLEWPEES 134

Q7 1 MEMLINSLALGAAVSAF.....FLDYVLELV NLEWPEES 134

Q7 1 MEMLINSLALGAAVSAF.....FLDYVLELV NLEWPEES 134

Q7 1 MEMLINSLALGAAVSAF.....FLDYVLELV NLEWPEES 134

Q7 1 MEMLINSLALGAAVSAF.....FLDYVLELV NLEWPEES 134

Q7 1 MEMLINSLALGAAVSAF.....FLDYVLELV NLEWPEES 134

Q7 1 MEMLINSLALGAAVSAF.....FLDYVLELV NLEWPEES 134

Q7 1 MEMLINSLALGAAVSAF.....FLDYVLELV NLEWPEES 134

Q7 1 MEMLINSLALGAAVSAF.....FLDYVLELV NLEWPEES 134

Q7 1 MEMLINSLALGAAVSAF.....FLDYVLELV NLEWPEES 134

Q7 1 MEMLINSLALGAAVSAF.....FLDYVLELV NLEWPEES 134

Q7 1 MEMLINSLALGAAVSAF.....FLDYVLELV NLEWPEES 134

G71914
 phosphatase phosphatase Helicobacter pylori (strain J99)
 C:Species: Helicobacter pylori
 A:Variant: strain J99
 C:Date: 12-Feb-1999 #sequence_revision: 12 Feb 1999 #text_change: 22 Jan 1999
 C:Accession: G71914
 K:Alm, K.A.; Hing, T.S.; Molt, D.; King, R.L.; Brown, E.H.; Doty, P.C.; Smith, D.R.;
 Lyons, C.J.; Gibson, P.; Moberg, P.; Mills, S.D.; Harg, V.; Taylor, D.E.; Vovis, G.F.;
 Nature 1997, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
 A:Reference number: A71800; MIMD:99120557; PMID:9923262
 A:Accession: G71914
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-207 -AAG-
 A:Cross-references: GB:AE001491; GB:AE001499; NID:94155127; FID:AA00170.1; FID:9415514
 A:Experimental source: strain J99
 A:Notes: seqB
 C:Superfamily: phosphoserine phosphatase

Query Match 10.4% Score 72.5; DB 2; Length 207;

Best Local Similarity 29.8%; Prod. No. 11;

Matches 31; Conservative 14; Mismatches 34; Indels 25; Gaps 5;

QY 9 ATCAAYSAVAE-NIMRVA EFLLSTHRTKGMNM 51

DB 109 LTRDAVRLTIVHNAKNTVHMNSYKTFMIAVFLINTEEELEVDCANL 158

QY 52 LPIPRVRRVCTFVLTALNTHRAVATLHNSLR 95

DB 159 LSRFVAV---VAVRAVETVPAH QYR PRALIK 204

RESULT 12

S33816

Kinesin light chain isoform 4 - sea urchin (Strongylocentrotus purpuratus)

C:Species: Strongylocentrotus purpuratus (purple urchin)

C:Date: 08-Dec-1993 #sequence_revision: 01-Dec-1995 #text_change: 09-Sep-1997

C:Accession: S33816

K:Wedeman, K.P.; Kuhlert, A.E.; Kendrick-Jones, J.; Scholey, J.M.

J. Mol. Biol. 231, 155-158, 1993

A:Title: Sequences of sea urchin kinesin light chain isoforms.

A:Reference number: S33813; MIMD:93267648; PMID:8496562

A:Accession: S33816

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-451 -MED-

A:Cross-references: EMBL:108258; NID:9415511; PID:9415532

Query Match 10.4% Score 72.5; DB 2; Length 451;

Best Local Similarity 25.9%; Prod. No. 28;

Matches 21; Conservative 19; Mismatches 30; Indels 11; Gaps 3;

QY 46 GGNLMITPKNKRLD LKFEACDITKNIAVAVKEPNSIKETPEYK 193

DB 15 GGNL-----NKKDITLKVHDKRNE-INKLNR 45

QY 104 KCACHEKVTKEIVLVAVL 124

DB 66 LVEKKDITKESLSSTHDA 86

RESULT 13

S33813

Kinesin light chain - sea urchin (Strongylocentrotus purpuratus)

C:Species: Strongylocentrotus purpuratus (purple urchin)

C:Date: 06-Jan-1995 #sequence_revision: 06-Jan-1995 #text_change: 09-Sep-1997

C:Accession: S33813

K:Wedeman, K.P.; Kuhlert, A.E.; Kendrick-Jones, J.; Scholey, J.M.

J. Mol. Biol. 241, 155-158, 1993

A:Title: Sequences of sea urchin kinesin light chain isoforms.

A:Reference number: S33813; MIMD:93267648; PMID:8496562

A:Accession: S33813

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-649 -MED-

A:Cross-references: EMBL:108258; NID:94155127; FID:9415514

Query Match

Best Local Similarity 25.9%; Prod. No. 44;

Matches 21; Conservative 19; Mismatches 30;

QY 46 GGNLMITPKNKRLD LKFEACDITKNIAVAVKEPNSIKETPEYK 193

DB 15 GGNL-----NKKDITLKVHDKRNE-INKLNR 45

QY 104 KCACHEKVTKEIVLVAVL 124

DB 66 LVEKKDITKESLSSTHDA 86

RESULT 14

S33814

Kinesin light chain - sea urchin (Strongylocentrotus purpuratus)

C:Species: Strongylocentrotus purpuratus (purple urchin)

C:Date: 06-Jan-1995 #sequence_revision: 01-Dec-1995 #text_change: 09-Sep-1997

C:Accession: S33814

K:Wedeman, K.P.; Kuhlert, A.E.; Kendrick-Jones, J.; Scholey, J.M.

J. Mol. Biol. 241, 155-158, 1993

A:Title: Sequences of sea urchin kinesin light chain isoforms.

A:Reference number: S33813; MIMD:93267648; PMID:8496562

A:Accession: S33814

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-677 -MED-

A:Cross-references: EMBL:108258; NID:94155127; FID:9415514

Query Match

Best Local Similarity 25.9%; Prod. No. 44;

Matches 21; Conservative 19; Mismatches 30;

QY 46 GGNLMITPKNKRLD LKFEACDITKNIAVAVKEPNSIKETPEYK 193

DB 15 GGNL-----NKKDITLKVHDKRNE-INKLNR 45

QY 104 KCACHEKVTKEIVLVAVL 124

DB 66 LVEKKDITKESLSSTHDA 86

RESULT 15

S33815

Kinesin light chain isoform 4 - sea urchin (Strongylocentrotus purpuratus)

C:Species: Strongylocentrotus purpuratus (purple urchin)

C:Date: 08-Dec-1993 #sequence_revision: 01-Dec-1995 #text_change: 09-Sep-1997

C:Accession: S33815; S36727

K:Wedeman, K.P.; Kuhlert, A.E.; Kendrick-Jones, J.; Scholey, J.M.

J. Mol. Biol. 241, 155-158, 1993

A:Title: Sequences of sea urchin kinesin light chain isoforms.

A:Reference number: S33813; MIMD:93267648; PMID:8496562

A:Accession: S33815

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-666 -MED-

A:Cross-references: EMBL:108258; NID:94155127; FID:9415514

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-666 -MED-

A:Cross-references: EMBL:108258; NID:94155127; FID:9415514

Query Match

Best Local Similarity 25.9%; Prod. No. 44;

Matches 21; Conservative 19; Mismatches 30;

115_121: GFLAVINIFWITE 144

RESULT 7

115_MERON

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IL5_MOUSE STANDARD: ERT 133 AA.
 AC P04601:
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-5 precursor (IL-5) (T-cell replacing factor) (TRF) (B-cell growth factor II) (BCGF-II) (Postnephil differentiation factor)
 DE Cytotoxic T lymphocyte inducer.
 GN IL5 OR IL-5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Camporelli R.D., Sanderson C.J., Wang Y., Holt Y., Marlinton M.E., Tucker W.O.J., Stetler-Stevenson G., Strath M., Young I.G., "Isolation, structure and expression of cDNA and genomic clones for murine eosinophil differentiation factor. Comparison with other eosinophilopoietic lymphokines and identity with interleukin-5.", J. Exp. Med. 174:345-352(1988).
 RL [2]
 RP SEQUENCE FROM N.A.
 RA Kishimoto T., Harada N., Severinson E., Tanabe T., Sideras P., Kishimoto M., Azuma G., Tomimaru A., Borstad-Lindqvist S., Takahashi M., Matsuda F., Yaela Y., Takatsu K., Honjo T., "Cloning of complementary DNA encoding T-cell replacing factor and identity with B-cell growth factor II.", Nature 324:70-73(1986).
 RL [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE:90180853; PubMed:3028564;
 PA Mizuta T.P., Tazuke T., Nakajima H., Nomi T., Honjo T., "Molecular cloning and structure of the mouse interleukin-5 gene.", Growth Factors 1:51-57(1988).
 RL [4]
 CC DEVELOPING B-CELLS TO IMMUNOLOGICAL SECRETING CELLS.
 CC -1- FUNCTION: FACTOR THAT INDUCES TERMINAL DIFFERENTIATION OF LATE
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IL-5 FAMILY.
 CC -----
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 CC -----
 DR EMBL: X06270; CAA29606.1;
 DR EMBL: X06271; CAA29697.1;
 DR EMBL: X04601; CAA28266.1;
 DR PIR: S00807; ICMS5.
 DR HSSP: P05113; 1H0L.
 DR MDL: M0196567; 115.
 DR InterPro: IPR000186; Interleukin_5.
 DR Pfam: PF02025; IL5_1.
 DR PRINTS: PR00432; INTERLEUKIN5.
 DR CYTOKINE: Growth factor; glycoprotein; signal.
 KW SIGNAL.
 FT CHAIN 1 20 INTERLEUKIN 5.
 FT DISULFID 62 62 INTERCHAIN WITH C 194 OR OTHER CHAIN
 FT DISULFID 104 104 (BY SIMILARITY).
 FT DISULFID 104 104 INTERCHAIN WITH C 62 OF OTHER CHAIN
 FT DISULFID 104 104 (BY SIMILARITY).
 FT CARBOHYD 46 46 N-LINKED (GLNAC...) (POTENTIAL).
 FT CARBOHYD 75 75 N-LINKED (GLNAC...) (POTENTIAL).
 FT CARBOHYD 89 89 N-LINKED (GLNAC...) (POTENTIAL).
 FT SIGNIFNT 133 AA. 15419 MW. 621542668 Da CD004.
 SD

Query Match: 14993 Score 476.16
 Best Local Similarity: 56.069 Ident. No. 8.7e-11
 Matches 75; Conservation 213 Mismatches 344
 2 EMBL: X06270; CAA29606.1; CAA29697.1; CAA28266.1; S00807; ICMS5; P05113; 1H0L; M0196567; 115; IPR000186; Interleukin_5; PF02025; IL5_1; IPR00432; INTERLEUKIN5; CYTOKINE: Growth factor; glycoprotein; signal; SIGNAL; CHAIN 1 20 INTERLEUKIN 5; DISULFID 62 62 INTERCHAIN WITH C 194 OR OTHER CHAIN; DISULFID 104 104 (BY SIMILARITY); DISULFID 104 104 INTERCHAIN WITH C 62 OF OTHER CHAIN; DISULFID 104 104 (BY SIMILARITY); CARBOHYD 46 46 N-LINKED (GLNAC...) (POTENTIAL); CARBOHYD 75 75 N-LINKED (GLNAC...) (POTENTIAL); CARBOHYD 89 89 N-LINKED (GLNAC...) (POTENTIAL); SIGNIFNT 133 AA. 15419 MW. 621542668 Da CD004.
 3 EMBL: X06270; CAA29606.1; CAA29697.1; CAA28266.1; S00807; ICMS5; P05113; 1H0L; M0196567; 115; IPR000186; Interleukin_5; PF02025; IL5_1; IPR00432; INTERLEUKIN5; CYTOKINE: Growth factor; glycoprotein; signal; SIGNAL; CHAIN 1 20 INTERLEUKIN 5; DISULFID 62 62 INTERCHAIN WITH C 194 OR OTHER CHAIN; DISULFID 104 104 (BY SIMILARITY); DISULFID 104 104 INTERCHAIN WITH C 62 OF OTHER CHAIN; DISULFID 104 104 (BY SIMILARITY); CARBOHYD 46 46 N-LINKED (GLNAC...) (POTENTIAL); CARBOHYD 75 75 N-LINKED (GLNAC...) (POTENTIAL); CARBOHYD 89 89 N-LINKED (GLNAC...) (POTENTIAL); SIGNIFNT 133 AA. 15419 MW. 621542668 Da CD004.
 62 INTERLEUKIN 5 precursor (IL-5) (T-cell replacing factor) (TRF) (B-cell growth factor II) (BCGF-II) (Postnephil differentiation factor)
 61 IL5 OR IL-5.
 122 FLAGWSTEWAME 132
 DB 121 FLAGWSTEWAME 132
 NRSUT 12
 IL5_MOUSE STANDARD: ERT 133 AA.
 AC P04601:
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
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 OX NCBI_Taxid=10090;
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 RP SEQUENCE FROM N.A.
 RA Camporelli R.D., Sanderson C.J., Wang Y., Holt Y., Marlinton M.E., Tucker W.O.J., Stetler-Stevenson G., Strath M., Young I.G., "Isolation, structure and expression of cDNA and genomic clones for murine eosinophil differentiation factor. Comparison with other eosinophilopoietic lymphokines and identity with interleukin-5.", J. Exp. Med. 174:345-352(1988).
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 RA Kishimoto T., Harada N., Severinson E., Tanabe T., Sideras P., Kishimoto M., Azuma G., Tomimaru A., Borstad-Lindqvist S., Takahashi M., Matsuda F., Yaela Y., Takatsu K., Honjo T., "Cloning of complementary DNA encoding T-cell replacing factor and identity with B-cell growth factor II.", Nature 324:70-73(1986).
 RL [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE:9432005; PubMed:3028564;
 PA Mizuta T.P., Tazuke T., Nakajima H., Nomi T., Honjo T., "Molecular cloning and structure of the mouse interleukin-5 gene.", Growth Factors 1:51-57(1988).
 RL [4]
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 CC -----
 DR EMBL: X06270; CAA29606.1;
 DR EMBL: X06271; CAA29697.1;
 DR EMBL: X04601; CAA28266.1;
 DR PIR: S00807; ICMS5.
 DR HSSP: P05113; 1H0L.
 DR MDL: M0196567; 115.
 DR InterPro: IPR000186; Interleukin_5.
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 FT CHAIN 1 20 INTERLEUKIN 5.
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 FT DISULFID 104 104 INTERCHAIN WITH C 62 OF OTHER CHAIN
 FT DISULFID 104 104 (BY SIMILARITY).
 FT CARBOHYD 46 46 N-LINKED (GLNAC...) (POTENTIAL).
 FT CARBOHYD 75 75 N-LINKED (GLNAC...) (POTENTIAL).
 FT CARBOHYD 89 89 N-LINKED (GLNAC...) (POTENTIAL).
 FT SIGNIFNT 133 AA. 15419 MW. 621542668 Da CD004.
 SD

Query Match: 73.143 Score 472.16
 Best Local Similarity: 56.069 Ident. No. 8.7e-11
 Matches 76; Conservation 213 Mismatches 344



GenCore version 5.1.3
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OM protein - protein search, using SW Model

Run on: November 8, 2002, 11:03:29, Search time 16.8193 Seconds
(without alignments)
589,721 Million cpul updaters/sec

Hit(s): US-09-755-633-5

Perfect score: 596
Sequence: 1 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134

Scoring table:

Gapop:10.0, Gapext:0.5

Searched: 671590 seqs, 20607115 residues

Total number of hits satisfying chosen parameters: 671590

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: SP_TREML_21:*
2: SP_Archaea:*
3: SP_Bacteria:*
4: SP_Fungi:*
5: SP_Human:*
6: SP_Invertebrate:*
7: SP_Mhc:*
8: SP_Mitochondria:*
9: SP_Phage:*
10: SP_Planct:*
11: SP_Rodent:*
12: SP_Virus:*
13: SP_Vertebrate:*
14: SP_Unclassified:*
15: SP_Virus:*
16: SP_Bacteriophage:*
17: SP_Archaea:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	696	100.0	134	095J76 Canis familiaris
2	586	84.2	134	095J76 Canis familiaris
3	578	83.0	134	095J76 Canis familiaris
4	571	82.0	118	095J76 Canis familiaris
5	354	50.9	134	095J76 Canis familiaris
6	109.5	15.7	40	095J76 Canis familiaris
7	79.5	11.4	258	095J76 Canis familiaris
8	78.5	11.3	258	095J76 Canis familiaris
9	78.5	11.3	463	095J76 Canis familiaris
10	78.5	11.3	490	095J76 Canis familiaris
11	77.5	11.1	331	095J76 Canis familiaris
12	77.5	11.1	428	095J76 Canis familiaris
13	76.5	10.8	490	095J76 Canis familiaris
14	75.5	10.8	490	095J76 Canis familiaris
15	75.5	10.8	490	095J76 Canis familiaris
16	74	10.6	241	095J76 Canis familiaris

17	74	10.6	241	095J76 Canis familiaris
18	74	10.6	241	095J76 Canis familiaris
19	73	10.6	241	095J76 Canis familiaris
20	73	10.5	191	095J76 Canis familiaris
21	73	10.5	241	095J76 Canis familiaris
22	72	10.5	241	095J76 Canis familiaris
23	73	10.5	241	095J76 Canis familiaris
24	73	10.5	241	095J76 Canis familiaris
25	72.5	10.4	241	095J76 Canis familiaris
26	72.5	10.4	241	095J76 Canis familiaris
27	72.5	10.4	241	095J76 Canis familiaris
28	72.5	10.4	241	095J76 Canis familiaris
29	72.5	10.4	241	095J76 Canis familiaris
30	72.5	10.4	241	095J76 Canis familiaris
31	72	10.3	241	095J76 Canis familiaris
32	71.5	10.3	241	095J76 Canis familiaris
33	71.5	10.3	241	095J76 Canis familiaris
34	71.5	10.3	241	095J76 Canis familiaris
35	71	10.2	241	095J76 Canis familiaris
36	71	10.2	241	095J76 Canis familiaris
37	71	10.2	241	095J76 Canis familiaris
38	71	10.2	241	095J76 Canis familiaris
39	71	10.2	241	095J76 Canis familiaris
40	71	10.2	241	095J76 Canis familiaris
41	71	10.2	241	095J76 Canis familiaris
42	71	10.2	241	095J76 Canis familiaris
43	70.5	10.1	241	095J76 Canis familiaris
44	70.5	10.1	241	095J76 Canis familiaris
45	70.5	10.1	241	095J76 Canis familiaris

ALIGNMENTS

RESULT 1

ID: 095J76 PRELIMINARY: ERT: 134 AA.

AC 095J76: MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134 AA.
DT 01-DEC-2001 (TREMBL) 134 (last sequence update)
DT 01-DEC-2001 (TREMBL) 134 (last sequence update)
DT 01-MAR-2002 (TREMBL) 134 (last annotation update)
DE Interleukin-5.
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Carnivora; Canidae.
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae.
OX NCBI_TaxID:9615;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE 2134438, PubMed 1141633;
FA Yang S, Salinas K.S., Weber E., McCall G.J.
ET "Canine Interleukin-5: A Novel Cytokine with
RT Expression of Biologically Active Recombinant Protein
DL J. Interleukin Cytokine Res. 21:761-767(2001).
DR EMBL: AF319420; AL007111;
DR FMBL: AF319419; AL007111;
DR InterPro: IPR001861; Interleukin_5.
DR Pfam: PF02025; I05.1.
SR SKIDANCE 134 AA: 150.000: 0040609400FF19

Query Match Best local Similarity: 100.000 Score: 696.0 DB: 134
Matches: 134; Conserved: 134; Mismatches: 0

09 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134
1 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134
2 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134
3 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134
4 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134
5 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134
6 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134
7 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134
8 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134
9 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134
10 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134
11 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134
12 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134
13 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134
14 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134
15 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134
16 MEMPHISALGCAVSAF.....FLDYQLVPLGV.NIEWTHS 134

DR EMH.; A113452; CAL
DR HSSP; 105113; 1HOL.

invertebrates (non-*Chordata*): Crustacea; Vertebrata: Euteleostomi;
Mammalia: Metazoa; Chordata: Craniata; Vertebrata: Euteleostomi;
Mammalia: Eutheria; Rodentia: Sciurognathi; Muridae: Murinae; Kallos.

[illegible]

01-MAR-2002 (11EMBLrel, 20, last sequence update)
 01-MAR-2002 (11EMBLrel, 20, last annotation update)
 005 Hypothetical 55.1 kDa protein
 008 Homo sapiens (human)
 009 Eukaryota; Metazoa; Chordata; Cephalata; Vertebrata; Euteleostomi;
 010 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
 011 NCBI TaxID 9606;
 012
 013 SEQUENCE FROM N.A.
 014 TISSUE LUNG;
 015 STRAUSBERG K;
 016 Submitted (06-2001) to the EMBL/GenBank/DDBJ databases.
 017 EMBL: B0017663; A017663.1;
 018 Hypothetical protein;
 019 SEQUENCE: 499 AA; 55897 MB; 22841332484200 08064;

Query Match 10.8%; Score 75.5; DB 4; Length 490;
 Best Local Similarity 22.1%; Prod. No. 24;
 Matches 42; Conservative 28; Mismatches 40; Indels 45; Gaps 6;

00 4 MLNLSLALZAVVSAFAVNRNRVATITLSTRTW 110 110 50
 100 153 MLNLSLALZAVVSAFAVNRNRVATITLSTRTW 110 110 50
 00 51 MIVVYVQNRH 510 510 100
 100 206 11 MIVVYVQNRH 510 510 100
 00 85 DKLFGNLSLFEHLEPQKRCVGR 109 109 50
 100 266 RQGLVWVTFLEPEKASMER 290 290 50

Search completed: November 8, 2002, 11:13:13
 Job Time : 50.8194 secs

ES claim 4b: Page 227, 24pp; English.

XX Sequences AAF58219-756226 represent encoded and mature
 CC canine interleukin-5 (IL-5). The invention relates to canine
 CC IL-4, canine or feline Fli-4 ligand, canine or feline GM0, canine or
 CC feline CD134 (GM040 ligand), canine IL-5, canine IL-13, feline
 CC interleukin-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumors, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense
 CC oligonucleotides). The proteins may be used to raise antibodies and to
 CC screen for modulators of activity, while the antibodies may be used in
 CC detection, and in drug targeting.

XX Sequence 115 AA:
 SU Query Match 100.0% Score 610; LR 21; Length 115;
 Best Local Similarity 100.0%; Pred. No. 6; Tr 6%;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 FAVENHNRVAVETITLSTHFWLTCRHWLMTTHNRCNRYGKENVYQITLKRQA 60
 DB 1 FAVENHNRVAVETITLSTHFWLTCRHWLMTTHNRCNRYGKENVYQITLKRQA 60

UY 61 HREAVDFEENSLFPHLECEPFEVCEPWYFEEVLELVYLVNINLWQES 115
 DB 61 HREAVDFEENSLFPHLECEPFEVCEPWYFEEVLELVYLVNINLWQES 115

RESULT 2
 ID AAF58219 standard; Protein: 134 AA.

XX AAF58219:
 DI 14-MAR-2000 (first entry)
 XX
 XX Canine interleukin-5 (IL-5).
 XX
 XX Interleukin-5, IL-5 antibody, canine inhibitor, immune response,
 XX immunoregulation; tumor; cancer; autoimmune disease; vaccine.
 XX
 XX Canis familiaris.

XX WO9961618-A2.

XX 02-Feb-1999.

XX 28-MAY-1999; 99WO-05811942.

XX 29-MAY-1998; 98US 0087305.

XX (HESK-1) HESKA 7063.

XX Sim G, Yang S, Drexler M, Wondolting RS;

XX WPI: 2000-07262736.

XX R 1568; AAF55546, AAF55547, AAF55548, AAF55549.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 XX useful for treating or preventing e.g. tumors or autoimmune disease

XX claim 4b: Page 224; 26pp; English.
 XX Sequences AAF58219-756226 represent encoded and mature

CC canine interleukin-5 (IL-5). The invention relates to canine
 CC IL-4, canine or feline Fli-4 ligand, canine or feline GM0, canine or
 CC feline CD134 (GM040 ligand), canine IL-5, canine IL-13, feline
 CC interleukin-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumors, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense
 CC oligonucleotides). The proteins may be used to raise antibodies and to
 CC screen for modulators of activity, while the antibodies may be used in
 CC detection, and in drug targeting.

XX Sequence 134 AA:
 SU Query Match 100.0% Score 610; LR 21; Length 134;
 Best Local Similarity 100.0%; Pred. No. 1; Tr 6%;
 Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 FAVENHNRVAVETITLSTHFWLTCRHWLMTTHNRCNRYGKENVYQITLKRQA 60
 DB 20 FAVENHNRVAVETITLSTHFWLTCRHWLMTTHNRCNRYGKENVYQITLKRQA 79

UY 61 HREAVDFEENSLFPHLECEPFEVCEPWYFEEVLELVYLVNINLWQES 115
 DB 80 HREAVDFEENSLFPHLECEPFEVCEPWYFEEVLELVYLVNINLWQES 134

RESULT 3
 ID AAF72615 standard; Protein: 134 AA.

XX AAF72615:
 DI 04-MAY-2001 (first entry)
 XX
 XX Canine interleukin-5 protein #1.
 XX
 XX Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
 XX inflammatory reaction.
 XX
 XX Canis sp.
 XX
 XX WO200111049-A2.

XX 15-FEB-2001.

XX 09-AUG-2000; 2000WO-0521651.

XX 10-AUG-1999; 99US-0371615.

XX (IDEX-1) IDEXX LAB INC.

XX Greg H, Lawton R, Mermet B, Alyssa Al;

XX WPI: 2001-191542/19.

XX N-PSIDG; AAF74300.

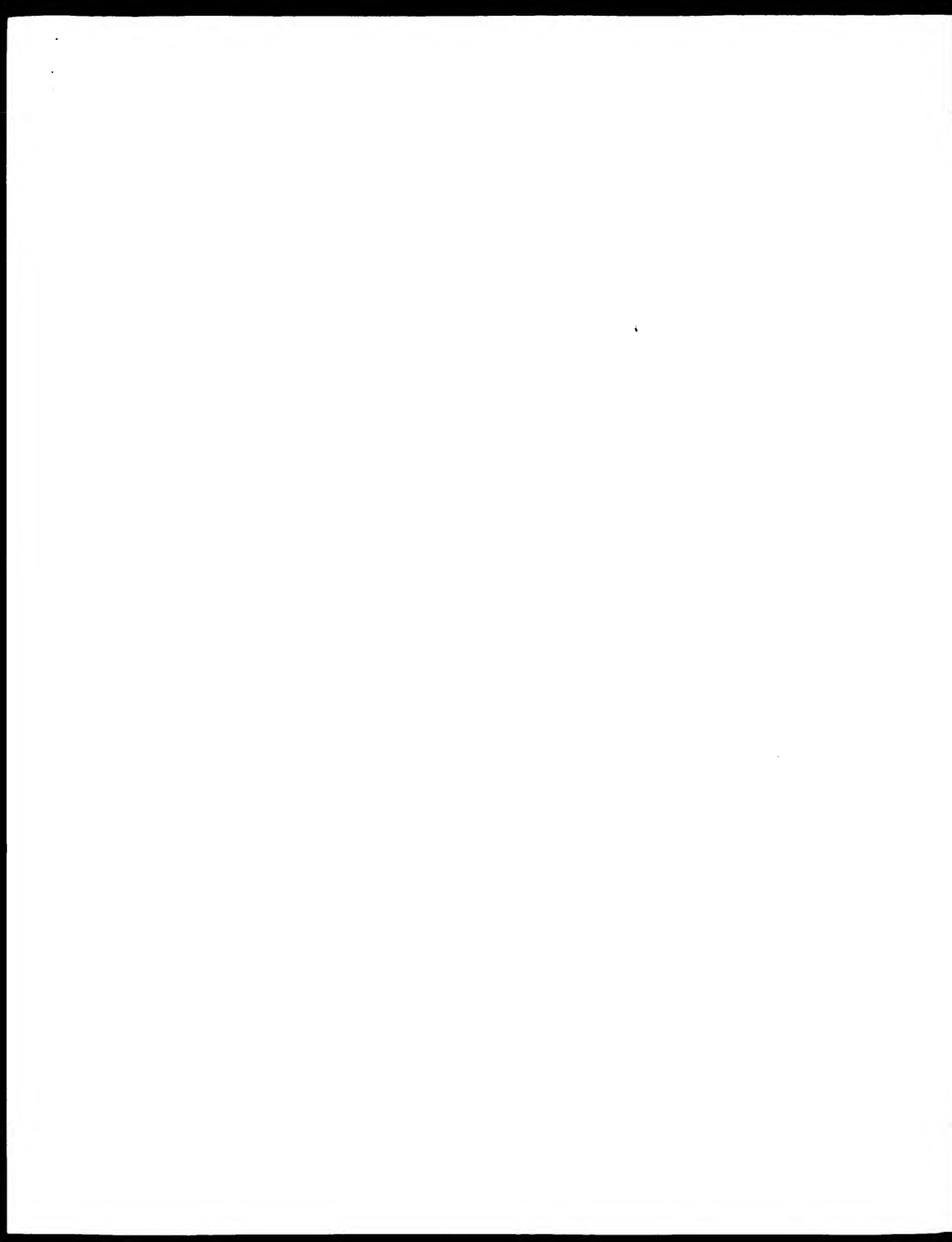
XX Novel canine interleukin-5 polynucleotide and polypeptides are used for
 XX generating antibodies which are useful in treating allergies in dogs

XX claim 24; Page 46-47; 48pp; English.

XX The present invention provides the protein and coding sequences of the
 XX canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
 XX cancer and inflammatory reactions in dogs. The present sequence is one
 XX variant of the IL-5 protein shown in the specification.

[illegible]

Page 1



GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: November 9, 2002, 11:09:04 : Search time 26.3213 Seconds
(without alignments)
544.033 Million cell updates/sec

Title: us-09-755-633-10

Perfect score: 610
Sequence: 1 FAVENPMNLVAETLTLST.....FTDYVQVFLGVINTEWTPES 115

Scoring table: HUSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96124122 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : PIR_731**
1: p1r1**
2: p1r2**
3: p1r3**
4: p1r4**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length on to	Description
1	491	80.5	134 2	JC5116
2	356	58.4	134 1	A28477
3	347	56.9	133 1	ICMS5
4	332	54.4	132 1	A48418
5	28.5	12.9	259 2	A47758
6	24.5	12.2	1232 2	B39432
7	23.5	12.0	253 2	A47757
8	22.5	11.9	253 2	CG5552
9	22.5	11.9	451 1	S33816
10	22.5	11.9	649 2	S33817
11	22.5	11.9	677 2	S33817
12	22.5	11.9	677 2	S33817
13	22.5	11.9	401 2	S29553
14	22.5	11.9	401 2	S29553
15	22.5	11.9	401 2	S29553
16	22.5	11.9	401 2	S29553
17	22.5	11.9	401 2	S29553
18	22.5	11.9	401 2	S29553
19	22.5	11.9	401 2	S29553
20	22.5	11.9	401 2	S29553
21	22.5	11.9	401 2	S29553
22	22.5	11.9	401 2	S29553
23	22.5	11.9	401 2	S29553
24	22.5	11.9	401 2	S29553
25	22.5	11.9	401 2	S29553
26	22.5	11.9	401 2	S29553
27	22.5	11.9	401 2	S29553
28	22.5	11.9	401 2	S29553
29	22.5	11.9	401 2	S29553

30	68.5	11.2	709 2	147089
31	68.5	11.2	1302 2	S65355
32	68	11.1	415 2	147254
33	68	11.1	414 2	147254
34	68	11.1	414 2	147254
35	68	11.1	767 1	106100
36	68	11.1	1955 2	110432
37	68	11.1	1621 2	A82455
38	67.5	11.1	1189 2	JCF118
39	67	11.0	415 2	147254
40	67	11.0	415 2	147254
41	67	11.0	415 2	147254
42	67	11.0	415 2	147254
43	66.5	10.9	274 2	121284
44	66.5	10.9	595 2	371377
45	66.5	10.9	767 2	147254

ALIGNMENTS

RESULT 1

JC5116 Interleukin-5 precursor - bovine

C1:Species: Bos primigenius taurus (cattle)

C1:Date: 02-Feb-1997 #sequence revision 27-Feb-1997 #1

C1:Accession: JC5116

R:Martens, B.; Gobright, E.; Shaw, B.F.

Gene 176, 273-274, 1996

A1>Title: The nucleotide sequence of the bovine interleukin-5 precursor

A1:Reference number: JC5116

A1:Accession: JC5116

A1:Accession: JC5116

A1:Accession: JC5116

A1:Accession: JC5116

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A1:Accession: JC5116

A1:Accession: JC5116

Cytokine 3, 72-81, 1991
A-Title: The rat inducible

A: Reference number: A48418; MUID: 91355638; PMID: 1653053

A;Accession: A48418
A;Status: preliminary

A: molecule type. DIA
A: residues: 1-132 (M)

A;C:Cross-references: EMBL

A;Note: sequential external

Order: Superfamily: Interleu-

Fig. 1-17, bottom: signal sequence #3 status predicted 210.
Fig. 1-19, top: signal sequence #4 status predicted 200.

F; 45, 74, 88, binding site. catalyzed

F761/disulfide bonds:	interchain (to 10)	#status predicted
F7103/disulfide bonds: <td>interchain (to 6)</td> <td>#status predicted</td>	interchain (to 6)	#status predicted

Index

Case	Year	Age	Sex	Site	Pathologic	Survival	Ref.
1	1971	50	F	Rectum	Adenocarcinoma	10 mo	[1]
2	1972	65	M	Rectum	Adenocarcinoma	10 mo	[2]
3	1973	60	F	Rectum	Adenocarcinoma	10 mo	[3]
4	1974	65	M	Rectum	Adenocarcinoma	10 mo	[4]
5	1975	60	F	Rectum	Adenocarcinoma	10 mo	[5]
6	1976	65	M	Rectum	Adenocarcinoma	10 mo	[6]
7	1977	60	F	Rectum	Adenocarcinoma	10 mo	[7]
8	1978	65	M	Rectum	Adenocarcinoma	10 mo	[8]
9	1979	60	F	Rectum	Adenocarcinoma	10 mo	[9]
10	1980	65	M	Rectum	Adenocarcinoma	10 mo	[10]
11	1981	60	F	Rectum	Adenocarcinoma	10 mo	[11]
12	1982	65	M	Rectum	Adenocarcinoma	10 mo	[12]
13	1983	60	F	Rectum	Adenocarcinoma	10 mo	[13]
14	1984	65	M	Rectum	Adenocarcinoma	10 mo	[14]
15	1985	60	F	Rectum	Adenocarcinoma	10 mo	[15]
16	1986	65	M	Rectum	Adenocarcinoma	10 mo	[16]
17	1987	60	F	Rectum	Adenocarcinoma	10 mo	[17]
18	1988	65	M	Rectum	Adenocarcinoma	10 mo	[18]
19	1989	60	F	Rectum	Adenocarcinoma	10 mo	[19]
20	1990	65	M	Rectum	Adenocarcinoma	10 mo	[20]
21	1991	60	F	Rectum	Adenocarcinoma	10 mo	[21]
22	1992	65	M	Rectum	Adenocarcinoma	10 mo	[22]
23	1993	60	F	Rectum	Adenocarcinoma	10 mo	[23]
24	1994	65	M	Rectum	Adenocarcinoma	10 mo	[24]
25	1995	60	F	Rectum	Adenocarcinoma	10 mo	[25]
26	1996	65	M	Rectum	Adenocarcinoma	10 mo	[26]
27	1997	60	F	Rectum	Adenocarcinoma	10 mo	[27]
28	1998	65	M	Rectum	Adenocarcinoma	10 mo	[28]
29	1999	60	F	Rectum	Adenocarcinoma	10 mo	[29]
30	2000	65	M	Rectum	Adenocarcinoma	10 mo	[30]
31	2001	60	F	Rectum	Adenocarcinoma	10 mo	[31]
32	2002	65	M	Rectum	Adenocarcinoma	10 mo	[32]
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34	2004	65	M	Rectum	Adenocarcinoma	10 mo	[34]
35	2005	60	F	Rectum	Adenocarcinoma	10 mo	[35]
36	2006	65	M	Rectum	Adenocarcinoma	10 mo	[36]
37	2007	60	F	Rectum	Adenocarcinoma	10 mo	[37]
38	2008	65	M	Rectum	Adenocarcinoma	10 mo	[38]
39	2009	60	F	Rectum	Adenocarcinoma	10 mo	[39]
40	2010	65	M	Rectum	Adenocarcinoma	10 mo	[40]
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42	2012	65	M	Rectum	Adenocarcinoma	10 mo	[42]
43	2013	60	F	Rectum	Adenocarcinoma	10 mo	[43]
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46	2016	65	M	Rectum	Adenocarcinoma	10 mo	[46]
47	2017	60	F	Rectum	Adenocarcinoma	10 mo	[47]
48	2018	65	M	Rectum	Adenocarcinoma	10 mo	[48]
49	2019	60	F	Rectum	Adenocarcinoma	10 mo	[49]
50	2020	65	M	Rectum	Adenocarcinoma	10 mo	[50]

Matches 14, conservative in, mismatches 11,

2 AVENIMPLVABEITLSTHPTWLEZENIMPTPENKHNHQTIR

1b 19 AMEIPMSTVKEETLIQSTHRAITSENFMPIPVPHKNHQIQSGEFOGELPIIKNOIVR 7

[illegible]

79 001VF1F0N1S1KKYTT00KFK07F00K0KTR001YU00E010V Db

RESULTS

hypothetical protein F2413.60 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-APR-2006 #Sequences: 100000000 #Taxa: 100000000

C; Accession: T47758

submitted to the Protein Sequence Database, February 20

A:Reference Number: 224475
A:Accession: 147758

A:Status: preliminary
A:Molecule type: RNA

A; Residues: 1-258 (NYA)

A: Cross-references: EMBL:AL138555
A: Experimental source: Cellar, Columbia, EDC and the EDC

C:Genetics:
A:Map position: 3

A: neutrons: 109/3

C; Superfamily: Arabidopsis thaliana hypothetical protein

[illegible]

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Model 6	26.8%	2.5
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Model 8	26.8%	2.5
Model 9	26.8%	2.5
Model 10	26.8%	2.5
Model 11	26.8%	2.5
Model 12	26.8%	2.5
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Model 97	26.8%	2.5
Model 98	26.8%	2.5
Model 99	26.8%	2.5
Model 100	26.8%	2.5

DATE	DESCRIPTION	AMOUNT
1967	CONSTRUCTION	100
1968	MISCELLANEOUS	50

9 PLVAFETLLESTHPIWICNBSHITFENINQLEEFVZLN
: || :: : | :|| :| : | : | : | : | : | : |

161 KAVANY ISTVASA... EGNEVNOZSSEKIHFIISIVLSOL

5. VERT. REL. FROM EQ. NO. 3 OF

111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 110

RESULT 6

ATP-dependent deoxyribonuclease chain A adda - Bacillus

N;Alternate names: Atp-dependent exonuclease synthesis
C;Species: *Bacillus subtilis*

C/Date: 21-Feb-1992 #80 photo_1992-106_01 Feb 1992 #200
C/Accession: R39433, H69582

Rijkolstra, J.; Venema, G.

100


```

RHS011 4
ID IL5_SHEEP STANDARD: PRI: 132 AA.
AC 028586;
DI 01-NOV-1997 (rel. 35, last sequence update)
DI 01-NOV-1997 (rel. 35, last annotation update)
DI 16-OCT-2001 (rel. 40, last annotation update)
DI Interleukin-5 precursor (IL-5) (T cell repelling factor) (TRF)
DE Interleukin-5 precursor (IL-5) (T cell repelling factor) (TRF)
DE (Eosinophil differentiation factor).
GN IL5.
OS Ovis aries (Sheep).
OC Artiodactyla; Cetartiodactyla; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae,
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID:9940;
RN (1)
RP SEQUENCE FROM N.A.
RA Bryson O.E., Viner E., Brandon M., Poyd A.W.;
RL Submitted (Jul-1995) to the EMBL/GenBank/DDBJ databases
[2]
RP SEQUENCE FROM N.A.
RA Seow H.F., David M.-J., McWaters P.G., Hurst L., Wood P.R.;
RL EMBL: 017053; AAB06293.1;
RL Submitted (Aug-1997) to the EMBL/GenBank/DDBJ databases
CC -1- FUNCTION: FACTOR THAT INDUCES TERMINAL DIFFERENTIATION OF LATE-
DEVELOPING B CELLS TO IMMUNOGLOBULIN SECRETING CELLS
(BY SIMILARITY).
CC -1- SOURCE: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-5 FAMILY.
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL collaboration.
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CC or send an email to license@sib-sb.ch.
CC
DR EMBL: 017053; AAB06293.1;
DR EMBL: 017053; AAB06293.1; J01IND.
DR EMBL: 035048; AAC99991.1; -
DR HSSP: P05113; IH01.
DR InterPro: IPR000186; Interleukin_5.
DR Pfam: PF02025; IL5; 1.
DR PRINTS: PR00432; INTERLEUKIN5.
DR CYCLINE: Growth factor; glycoprotein; signal.
FT SIGNAL 1 19
FT CHAIN 20 132 INTERLEUKIN 5.
FT DISULFID 61 61 INTERCHAIN (WITH C 103 OF OTHER CHAIN)
FT DISULFID 103 103 INTERCHAIN (WITH C-61 OF OTHER CHAIN)
FT DISULFID 103 103 INTERCHAIN (WITH C-61 OF OTHER CHAIN)
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Query Match 79.8% Score 487. DB 1; Length 132;
Best Local Similarity 90.7% Pred. No. 4,2e-43;
Matches 92; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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AC 008967;
DI 15-DEC-1998 (rel. 37, created)
DI 15-DEC-1998 (rel. 37, last sequence update)
DI 16-OCT-2001 (rel. 40, last annotation update)
DI Interleukin 5 precursor (IL-5) (T cell repelling factor)
DE (Eosinophil differentiation factor).
GN IL5.
OS Canis porcellus (Guinea Pig).
OC Dikaryota; Actinoptera; Chordata; Vertebrata
OC Mammalia; Eutheria; Rodentia; Muricolonathina; Canis
OX NCBI_TaxID:10141;
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE:96289181; PMID:974122;
RA Mansour M., Kallianiotis M., Hsu J.H.S.J., Nasser
RA Conklyn M.D., Lilly C.M., Huzar J.M., Lee S.H.,
RA de Wet J.R., Cohen V.L., Stewart H.J., Hanley J.P.
PT "production and characterization of guinea pig IL
AT infected insect cells."
RL Am. J. Physiol. 270:R1102-R1107 (1996).
CC -1- FUNCTION: FACTOR THAT INDUCES TERMINAL DIFFEREN
DEVELOPING B-CELLS TO IMMUNOGLOBULIN SECRETING
(BY SIMILARITY).
CC -1- SOURCE: HOMO-DIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-5 FAMILY.
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL collaboration.
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CC
DR EMBL: 034588; AAB03457.1
DR HSSP: P05113; IH01.
DR InterPro: IPR000186; Interleukin_5.
DR Pfam: PF02025; IL5; 1.
DR PRINTS: PR00432; INTERLEUKIN5.
DR CYCLINE: Growth factor; glycoprotein; signal.
FT SIGNAL 1 19
FT CHAIN 20 132 INTERLEUKIN 5.
FT DISULFID 64 64 INTERCHAIN (WITH C-61 OF OTHER CHAIN)
FT DISULFID 106 106 INTERCHAIN (WITH C-61 OF OTHER CHAIN)
FT CARBOHYD 48 48 N-LINKED (GLYCAN...) (CONTINUED)
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Best Local Similarity 60.9% Pred. No. 2.7e-41;
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ID IL5_CAVPO STANDARD: PRI: 145 AA.
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DE (Eosinophil differentiation factor).
GN IL5.
OS Canis porcellus (Guinea Pig).
OC Dikaryota; Actinoptera; Chordata; Vertebrata
OC Mammalia; Eutheria; Rodentia; Muricolonathina; Canis
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RA MEDLINE:96289181; PMID:974122;
RA Mansour M., Kallianiotis M., Hsu J.H.S.J., Nasser
RA Conklyn M.D., Lilly C.M., Huzar J.M., Lee S.H.,
RA de Wet J.R., Cohen V.L., Stewart H.J., Hanley J.P.
PT "production and characterization of guinea pig IL
AT infected insect cells."
RL Am. J. Physiol. 270:R1102-R1107 (1996).
CC -1- FUNCTION: FACTOR THAT INDUCES TERMINAL DIFFEREN
DEVELOPING B-CELLS TO IMMUNOGLOBULIN SECRETING
(BY SIMILARITY).
CC -1- SOURCE: HOMO-DIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-5 FAMILY.
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
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CC
DR EMBL: 034588; AAB03457.1
DR HSSP: P05113; IH01.
DR InterPro: IPR000186; Interleukin_5.
DR Pfam: PF02025; IL5; 1.
DR PRINTS: PR00432; INTERLEUKIN5.
DR CYCLINE: Growth factor; glycoprotein; signal.
FT SIGNAL 1 19
FT CHAIN 20 132 INTERLEUKIN 5.
FT DISULFID 64 64 INTERCHAIN (WITH C-61 OF OTHER CHAIN)
FT DISULFID 106 106 INTERCHAIN (WITH C-61 OF OTHER CHAIN)
FT CARBOHYD 48 48 N-LINKED (GLYCAN...) (CONTINUED)
FT CARBOHYD 77 77 N-LINKED (GLYCAN...) (CONTINUED)
FT CARBOHYD 91 91 N-LINKED (GLYCAN...) (CONTINUED)
SU SEQUENCE 135 AA; 15291 MW; 188525212F52741 GP

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For entities requiring a license agreement, the fee for such an agreement is \$1000.

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[illegible]

The first part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The second part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The third part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The fourth part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The fifth part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The sixth part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The seventh part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The eighth part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The ninth part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

The tenth part of the paper discusses the importance of maintaining accurate records of all transactions. It is essential for the company to have a clear and concise record of all financial activities, including sales, purchases, and expenses. This will allow the company to track its performance over time and identify areas for improvement.

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EM protein - protein search, using SW model

Run on: November 8, 2002, 11:02:28 : Search time 40.1807 seconds
(without alignments)
589,721 Million cell updates/sec

Title: US-09-755-633-10

Perfect score: 610

Sequence: 1 FAVINSEMEIVAEIILILIST.....FELTGVETLVVILWETTES 115

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 205047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum hit seq length: 6

Maximum hit seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: SP_ARCHA: *
2: SP_BACTERIA: *
3: SP_FUNGI: *
4: SP_HUMAN: *
5: SP_INVERTEBRATE: *
6: SP_MAMMAL: *
7: SP_MOUSE: *
8: SP_ORNITHO: *
9: SP_PLANT: *
10: SP_PROTOZOA: *
11: SP_VIRUS: *
12: SP_VIRUS: *
13: SP_VIRUS: *
14: SP_VIRUS: *
15: SP_VIRUS: *
16: SP_VIRUS: *
17: SP_VIRUS: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	Hit ID	Description
1	610	100.0	134	6	Q95J76 canis fam1
2	568	92.3	118	6	Q9LV10 canis fam1
3	505	82.8	134	6	Q9LSD7 felis silve
4	501	82.1	134	6	Q9MYM5 mus muscu
5	425	53.3	132	11	Q9P229 felis silve
6	409.5	51.0	40	6	Q9X192 canis fam1
7	39.5	12.9	258	10	Q9X192 canis fam1
8	39.5	12.5	158	5	Q96575 leucophaea
9	39.5	12.0	253	10	Q96575 leucophaea
10	39.5	12.0	191	11	Q96575 leucophaea
11	39.5	12.0	248	10	Q96575 leucophaea
12	39.5	12.0	661	11	Q92125 mus muscu
13	39.5	11.9	229	10	Q92125 mus muscu
14	39.5	11.9	418	10	Q92125 mus muscu
15	39.5	11.9	296	10	Q92125 mus muscu
16	39.5	11.7	823	5	Q9X226 canis fam1

17	71	11.6	253	10	Q96575 leucophaea
18	71	11.6	418	10	Q96575 leucophaea
19	71	11.6	418	10	Q96575 leucophaea
20	71	11.6	418	10	Q96575 leucophaea
21	71	11.6	418	10	Q96575 leucophaea
22	70.5	11.6	418	10	Q96575 leucophaea
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ALIGNMENTS

RESULT 1	Q95J76	PRELIMINARY	114	114	AA
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AC	Q95J76	PRELIMINARY	114	114	AA
DT	01-DEC-2001 (FEMH) rev. 1.0 (revised)				
DT	01-DEC-2001 (FEMH) rev. 1.0 (revised)				
DT	01-MAR-2002 (FEMH) rev. 1.0 (revised)				
DE	Interleukin-5				
OS	Canis familiaris (dog)				
OC	Eukaryota; Metazoa; Chordata; Carnivora; Canidae				
OC	Mammalia; Canidae; Carnivora; Canidae				
OX	NCBI_TaxID:9615				
RN	[1]				
RP	SEQUENCE FROM N.A.				
FX	MEDLINE:2134408; PubMed:114114				
SA	Interleukin-5 is a secreted protein that is				
RT	expression of biologically active recombinant pro-				
RL	J. Interleukin Cytokine Receptor 2134408 (2001)				
DR	FEMH: AF331920; AAT:114114				
DR	FEMH: AF331920; AAT:114114				
DR	InterPro: IPR000261; AAT:114114				
DR	Tram: PF02027; IPR:114114				
SQ	SEQUENCE 114 AA; 1500 MW; 30.00009439 E11.0				
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Best Local Similarity	114	Score 610	114		
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1	FAVINSEMEIVAEIILILIST.....FELTGVETLVVILWETTES				
2	FAVINSEMEIVAEIILILIST.....FELTGVETLVVILWETTES				
3	FAVINSEMEIVAEIILILIST.....FELTGVETLVVILWETTES				
4	FAVINSEMEIVAEIILILIST.....FELTGVETLVVILWETTES				
5	FAVINSEMEIVAEIILILIST.....FELTGVETLVVILWETTES				
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7	FAVINSEMEIVAEIILILIST.....FELTGVETLVVILWETTES				
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16	FAVINSEMEIVAEIILILIST.....FELTGVETLVVILWETTES				

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07	1	FAVNIHRSVATGTTTAASTHRTWLTGWRMLTITLAKNSGLSEVTVLSTITLPLDIA	61	118
10	8	FAVNIHRSVATGTTTAASTHRTWLTGWRMLTITLAKNSGLSEVTVLSTITLPLDIA	61	118
09	61	HDEAVLEPLTKEQLEFEEETPEALGDSVATGTTTAASTHRTWLTGWRMLTITLAKNSGLSEVTVLSTITLPLDIA	118	118
10	68	HDEAVLEPLTKEQLEFEEETPEALGDSVATGTTTAASTHRTWLTGWRMLTITLAKNSGLSEVTVLSTITLPLDIA	118	118

[illegible][illegible][illegible]

Fri NOV 8 12:51:26 2002

us-09-755-633-5.ra1

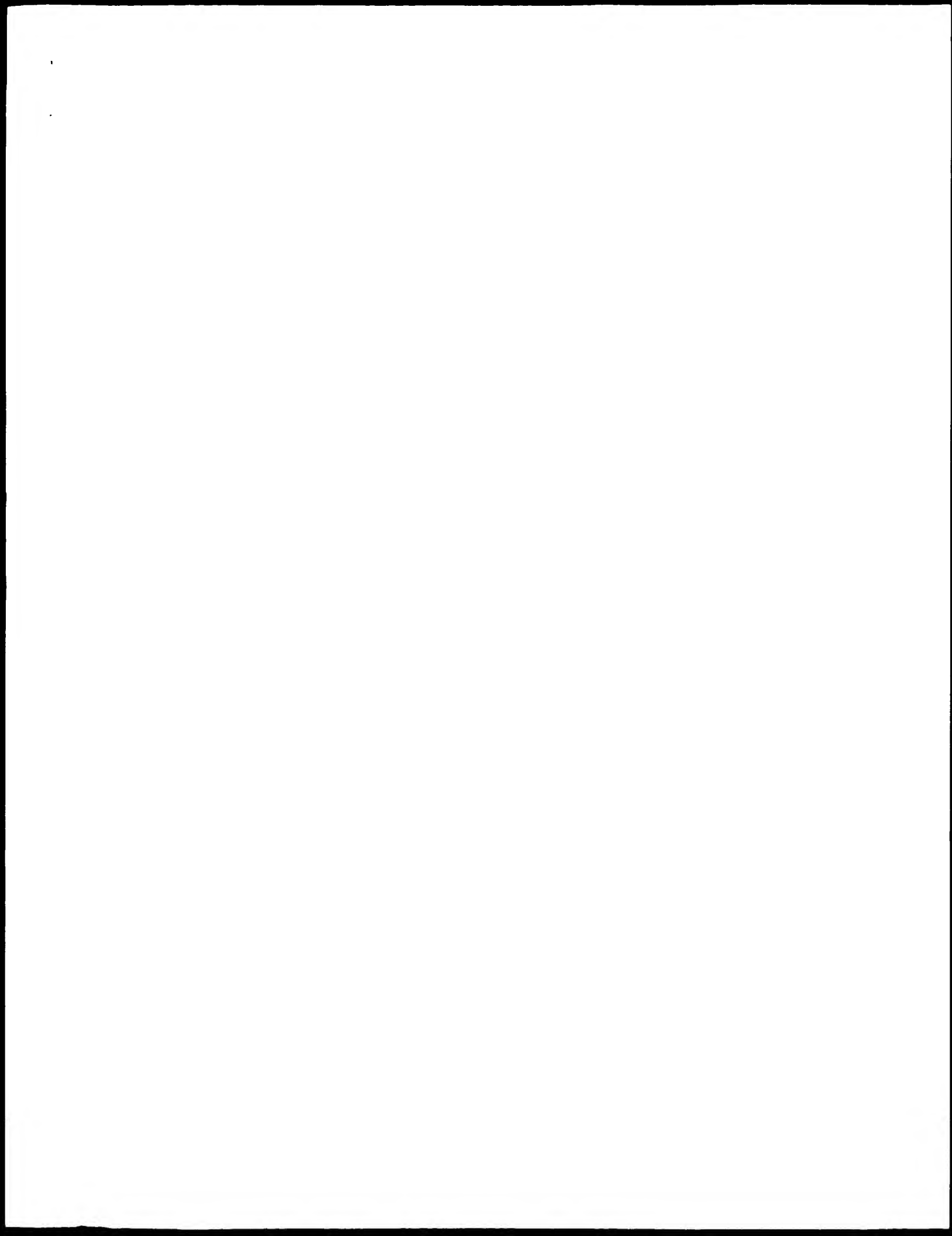
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1 CORRESPONDENCE ADDRESS:
2 ADDRESSEE: MERCHANT & COULD
3 STREET: 4100 NO. 6218162west Center, 40 South Seventh Street
4 CITY: Minneapolis
5 STATE: Minnesota
6 COUNTRY: U.S.A.
7 ZIP: 55402-4131
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC compatible
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 SOFTWARE: Patent in release #1.0, Version #1.30
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: 05/08764, 678
15 FILING DATE: 14-JUN-1996
16 CLASSIFICATION: 445
17 ATTORNEY/AGENT INFORMATION:
18 NAME: Mueller, Douglas P.
19 REGISTRATION NUMBER: 30,300
20 REFERENCE/WORKER NUMBER: 967 7933 49-00-01
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: 612-332-5400
23 TELEFAX: 612-332-4081
24 INFORMATION FOR SEQ. ID NO.: 8:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 1187 amino acids
27 TYPE: amino acid
28 Topology: linear
29 MOLECULE TYPE: protein
30 US-08-664-9648-H
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32 Query Match 10.08; Score 69.5; DB 4; Length 1187;
33 best local similarity 28.38; Pred. No. 10;
34 Matches 27; Conserved 26; Mismatches 50; E.A.S. 13; Gaps 5;
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36 02 VENMNPLVETIIITLTHPTWIDHNMPTTPKPKNGCTEVDVGI-DIKKSTAR 80
37 464 LPHSLGPTISVTYVAAILKMLKLVAVAKELHLSHSGTHVAGCTATLGGKAV 522
38 523 G-VSEHFNIGTSCHEVERL 702SERLKNKQNTNNTNIALDNLAP 570
39
40 RESULT 11
41 US-09-411-743-H
42 Sequence 8, Application 05/09311743
43 Patent No. 6248903
44 GENERAL INFORMATION:
45 APPLICANT: Krystal, Gerald
46 TITLE OF INVENTION: SH2-CONTAINING INHIBIT-PROPHATASE
47 NUMBER OF SEQUENCES: 24
48 CORRESPONDENCE ADDRESS:
49 ADDRESSEE: APPERTIN & PAPP
50 STREET: 40 King Street West
51 CITY: Toronto
52 STATE: Ontario
53 COUNTRY: Canada
54 ZIP: M5H 3Y2
55 COMPUTER READABLE FORM:
56 MEDIUM TYPE: Floppy disk
57 COMPUTER: IBM PC compatible
58 OPERATING SYSTEM: PC-DOS/MS-DOS
59 SOFTWARE: Patent in release #1.0, Version #1.30
60 CURRENT APPLICATION DATA:
61 APPLICATION NUMBER: 05/09311, 743
62 FILING DATE: 14-May-1999
63 CLASSIFICATION: <00knew>
64 ATTORNEY/AGENT INFORMATION:
65 NAME: Gravello, Michelino
66 REGISTRATION NUMBER: 40,261
67 REFERENCE/WORKER NUMBER: 7793-02
68 TELECOMMUNICATION INFORMATION:

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1 2 TELEPHONE: 415-471-1700
3 3 TELEFAX: 415-471-1700
5 4 INFORMATION FOR SEQ. 11 NO. 80
7 5 SEQUENCE CHARACTERISTICS
9 6 LENGTH: 1100 BASE PAIRS
11 7 TYPE: DNA; POS. 1
13 8 TOPOLOGY: CIRCULAR
15 9 MOLECULE TYPE: PROTEIN
17 10 SEQUENCE DESCRIPTION: PROTEIN NO. 80
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GenCore version 5.1.3
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COM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 09:51:15 : Search Time 1730.26 Seconds
(without alignment)

102600 Ith Million reqs/updates/sec

Title: US-09-755-633-4

Perfect score.	610
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Sequence: 1 caaaggcaaacctgacatt.....accagatgaaatatatttgaag 610

Scoring table: `OLIGO_NJC`

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of files satisfying chosen parameters. 4109280

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Minimum PB seq length: 0
Maximum PB seq length: 20000000000
```

Maximum LB seq length: 2000000000

Post-processing: listing first 15 summaries

Palabasc :

1:	qb_bay.*
2:	qb_hug.*
3:	qb_in.*
4:	qb_om.*
5:	qb_ov.*
6:	qb_pat.*
7:	qb_ph.*
8:	qb_pl.*
9:	qb_pt.*
10:	qb_ro.*
11:	qb_scs.*
12:	qb_sy.*
13:	qb_un.*
14:	qb_vt.*
15:	ac_ba.*
16:	em_hum.*
17:	em_hum.*
18:	em_in.*
19:	em_om.*
20:	em_om.*
21:	em_pt.*
22:	em_pt.*
23:	em_pat.*
24:	em_ph.*
25:	em_pl.*
26:	em_ro.*
27:	em_scs.*
28:	em_un.*
29:	em_vt.*
30:	em_hug_hum.*
31:	em_hug_in.*
32:	em_hug_other.*
33:	em_hug_om.*
34:	em_hug_ph.*
35:	em_hug_pt.*
36:	em_hug_qm.*
37:	em_hug_vt.*
38:	em_sy.*
39:	em_hqo_hum.*
40:	em_hqo_must.*
41:	em_hqo_other.*

Pred. 13. is the number of results predicted by chance to have a

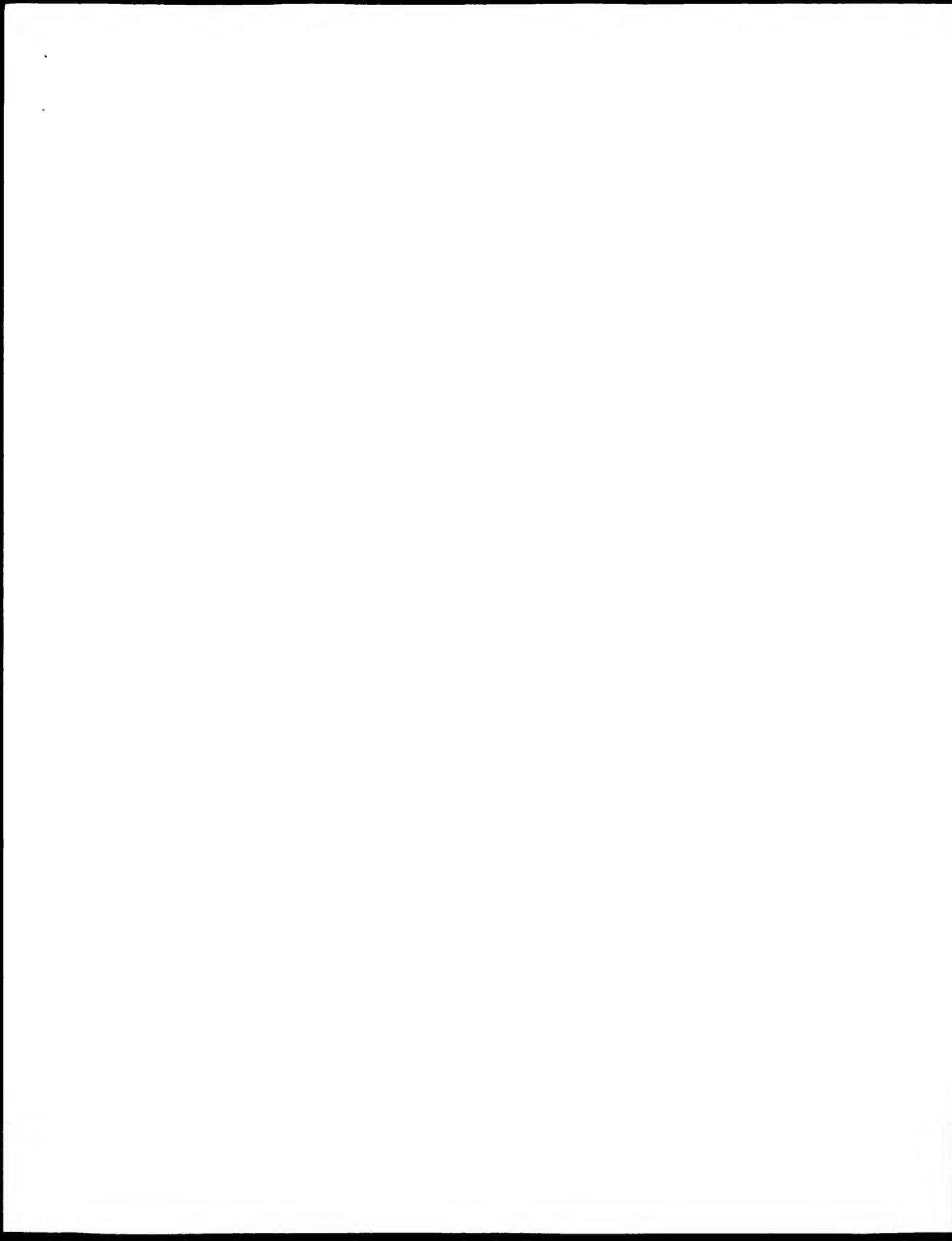
score greater than or equal to the score of T_{max} and is derived by analysis of the total score d .

SUMMARY

Result	No.	Score	Query Match	Length	Id
	1	610	100.0	610	AF001819
	2	593	94.4	428	AA003939
	3	271	44.4	474	AF001133
	4	250	41.0	343	AX003948
	5	170	27.9	167	AF001620
	6	43	7.0	520	AF005048
	7	43	7.0	1145	GA011041
	8	42	6.9	405	SS001608
	9	41	6.9	409	SS001345
	10	41	6.7	405	AF006770
	11	41	6.7	405	AF001500
	12	41	6.7	404	AF025446
	13	40	6.6	405	EF001947
	14	30	4.9	414	AF051372
	15	29	4.6	17	AF001356
	16	28	4.6	543	EF003539
	17	28	4.6	227	EF00768
	18	22	3.6	42	EF01456
	19	22	3.6	45	EF0155A
	20	22	3.6	405	EF019448
	21	22	3.6	421	SS00115A
	22	22	3.6	459	AF001032
	23	22	3.6	709	AF002850
	24	22	3.6	816	EF00639
	25	22	3.6	815	EF00591
	26	22	3.6	816	HS0115R
	27	22	3.6	816	AF00101A
	28	22	3.6	816	AF006275
	29	22	3.6	720	EF00540
	30	22	3.6	420	EF00592
	31	22	3.6	420	HS00101R
	32	22	3.6	420	HM00115
	33	22	3.6	421	HM00115A
	34	22	3.6	421	HM00115R
	35	22	3.6	446	PF00105R
	36	22	3.6	446	AF003245
	37	22	3.6	521	AF004692
	38	22	3.6	1636	AF007930
	39	22	3.6	1694	AF011633
	40	21	3.4	64	AF007306
	41	21	3.4	470	AA00450
	42	21	3.4	470	AA00451
	43	21	3.4	475	AF00711
	44	21	3.4	475	AF00765
	45	21	3.4	477	AF007188

CONCLUSION

RESULT 1	AF331919	610 bp	mRNA
LOCUS	AF331919		
DEFINITION	Canis familiaris 5' end of the 12S rRNA gene		
ACCESSION	AF331919		
VERSION	AF331919.1	01-15-2000	
KEYWORDS			
SOURCE	Canis familiaris		
ORGANISM	Canis familiaris		
	Eukaryota; Metazoa; Chordata; Carnivora; Mammalia; Euphrasia; Canivora; Fissipedia; 1 (bases 1 to 610)		
REFERENCE	Yano, S., Saitoh, K., Weber, E., and Mochizuki, T. 1999. Molecular characterization of the 12S rRNA gene expression in the developing ovine embryo.		
AUTHORS			
TITLE			



Matches 12: Conservative 10: Mismatches 9: Indels 0: Gaps 0:

QY 45 ATTGAGTTTGGTACCTCTGG 66

DB 1 AAGGAGAGAGAGAGAGAGAGAG 22

RESULT 2

US-08-466-852-2

Sequence 2, Application US/08466852

Patent No. 5681936

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: A SINGLE STEP PURIFICATION OF

TITLE OF INVENTION: RECOMBINANT HUMAN INTERLEUKIN 5

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 East Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: USA

ZIP: 07065-0907

COMPUTER PEADABLE: yes

MEDIUM TYPE: Diskette, 3.5 in, 1.4Kb

COMPUTER: Apple Macintosh

OPERATING SYSTEM: System 7.0.1

SOFTWARE: Microsoft Word 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 05/05/466,852

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Panzer, Curtis C.

REGISTRATION NUMBER: 33,752

REFERENCE/DOCKET NUMBER: 19151A

TELEPHONE: (908)594 3199

TELEFAX: (908)594 4720

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 47 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-466-852-2

Query Match 3.6% Score 22: DB 1: Length 47:

Best Local Similarity 100.0%: Prod. No. 0.11:

Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 45 ATTGAGTTTGGTACCTCTGG 66

DB 29 ATTGAGTTTGGTACCTCTGG 8

RESULT 3

US-09-079-839-2

Sequence 2, Application US/09079839

Patent No. 6048726

GENERAL INFORMATION:

APPLICANT: Weisman, Joel K.

TITLE OF INVENTION: INHIBITION OF EOSINOPHILIC INFLAMMATION

FILE REFERENCE: 09698/002001

CURRENT APPLICATION NUMBER: US-09-079,839

CURRENT FILING DATE: 1999-05-15

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 2

LENGTH: 816

TYPE: DNA

ORGANISM: Homo sapiens

US-09-079-839-2

Query Match

Best Local Similarity 100.0%: Prod. No. 0.11:

Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 45 ATTGAGTTTGGTACCTCTGG 66

DB 61 ATTGAGTTTGGTACCTCTGG 82

RESULT 4

US-09-280-799-78

Sequence 78, Application US/09280799

Patent No. 6136603

GENERAL INFORMATION:

APPLICANT: Dean, Nicholas M.

APPLICANT: Karras, James G.

APPLICANT: McKay, Robert

TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN-5 SIGNAL

FILE REFERENCE: ISPH-0340

CURRENT APPLICATION NUMBER: 05/05/280,799

CURRENT FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 208

SOFTWARE: patentin ver. 2.0

SEQ ID NO 78

LENGTH: 3230

TYPE: DNA

ORGANISM: Homo sapiens

US-09-280-799-78

Query Match 3.6% Score 22: DB 3: Length 3230:

Best Local Similarity 100.0%: Prod. No. 0.11:

Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 45 ATTGAGTTTGGTACCTCTGG 66

DB 569 ATTGAGTTTGGTACCTCTGG 590

RESULT 5

US-09-640-1

Patent No. 5324640

APPLICANT: Hecio, Tasuku; Tatey, Kinshi; Sevelin, Eva

TITLE OF INVENTION: HUMAN B-CELL DIFFERENTIATION FACTOR AND

PROCESS OF PRODUCING SAID FACTOR

NUMBER OF SEQUENCES: 2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/79,467

FILING DATE: 21-SEP-1987

SEQ ID NO: 1

LENGTH: 3230

US-09-640-1

Query Match 3.6% Score 22: DB 3: Length 3230:

Best Local Similarity 100.0%: Prod. No. 0.11:

Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 45 ATTGAGTTTGGTACCTCTGG 66

DB 569 ATTGAGTTTGGTACCTCTGG 590

RESULT 6

US-09-100-064-1

Sequence 1, Application US/09100864

Patent No. 6465616

GENERAL INFORMATION:

APPLICANT: Lopez, Angel

APPLICANT: Vadas, Matthew

APPLICANT: Shannon, Frances

NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MOTOR & CO., INC.
 STREET: 126 East Lincoln Avenue
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07065-0907
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 4.5 in, 1.44K
 OPERATING SYSTEM: System 7.0.1
 SOFTWARE: Microsoft Word 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/755, 952
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT: US/09/755
 NAME: Patrick, Cathie C.
 REGISTRATION NUMBER: 33,752
 REFERENCE/AGENT NUMBER: 199511A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908)594-8199
 TELEFAX: (908)594-1720
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 39 bases
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-466-852-1

Query Match: 2.8%; Score 17; DB 1; Length 39;
 Best Local Similarity: 100.0%; Prod. No. 44;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 ATTGAGTTGCTACT 61
 DB 24 ATTGAGTTGCTACT 39

RESULT 10
 US-09-428-111-666
 Sequence 666, Application US/09/29111
 Patent No. 6262333
 GENERAL INFORMATION:
 ADDRESSEE: Fudoge, Wilson O.
 APPLICANT: Steinmann, Kathleen E.
 APPLICANT: Astle, Jon H.
 APPLICANT: Burgess, Christopher O.
 APPLICANT: Bushnell, Steven E.
 APPLICANT: Carroll III, Eddie
 APPLICANT: Catino, Theodore J.
 APPLICANT: Dettl, Adrian
 APPLICANT: Ford, Donna M.
 APPLICANT: Lewis, Marcia E.
 APPLICANT: Monahan, John E.
 APPLICANT: Schlegel, Robert
 TITLE OF INVENTION: HEAVY HUMAN GLOBIN GENES AND GLOBE EXPRESSION
 TITLE OF INVENTION: PRODUCTS
 FILE REFERENCE: CDD-257 (US)
 CURRENT APPLICATION NUMBER: US/09/29111
 CURRENT FILING DATE: 1999-06-08
 EARLIER APPLICATION NUMBER: US 60/209,801
 EARLIER FILING DATE: 1998-04-10
 NUMBER OF SEQ ID NOS: 850
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 666
 LENGTH: 449
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-428-111-666

Query Match: 2.8%; Score 17; DB 4; Length 449;
 Best Local Similarity: 100.0%; Prod. No. 44;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 AGCTGTCATTAACCTA 289
 DB 192 AGCTGTCATTAACCTA 208

RESULT 11
 US-09-280-116-171
 Sequence 171, Application US/09/280116A
 Patent No. 6331427
 GENERAL INFORMATION:
 ADDRESSEE: Robinson, Keith E.
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES INCODING HUMAN PROTEASE HEMOLASIN
 FILE REFERENCE: SEQ ID NO 24, US/09/276965
 CURRENT APPLICATION NUMBER: US/09/280,116A
 CURRENT FILING DATE: 1999-04-26
 NUMBER OF SEQ ID NOS: 268
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 171
 LENGTH: 823
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: PROLYL OLIGOPROTEIDASES
 US-09-280-116-171

Query Match: 2.8%; Score 17; DB 4; Length 823;
 Best Local Similarity: 100.0%; Prod. No. 44;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 CTACTCTGAAATATAA 202
 DB 681 CTACTCTGAAATATAA 697

RESULT 12
 US-09-049-137-176
 Sequence 1, Application US/09/049137
 Patent No. 5856157
 GENERAL INFORMATION:
 ADDRESSEE: Schaff, David
 APPLICANT: Craig, Richard
 APPLICANT: Medford, June L.
 APPLICANT: Manno, R.O.
 APPLICANT: Cox-Foster, Diana L.
 TITLE OF INVENTION: A No. 5856157-1 by 14:0-ACP Fatty
 TITLE OF INVENTION: Acid Desaturase and Gene Therator
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: The Webb Law Firm
 STREET: 700 Koppers Building, 446 South Avenue
 CITY: Pittsburgh
 STATE: PA
 COUNTRY: USA
 ZIP: 15219-1818
 MEDIUM TYPE: Diskette
 MEDIUM TYPE: 3.5 in, 1.44K
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 5856157, 157
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 62/018,957
 FILING DATE: 04-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Johnson, Barbara E

REGISTRATION NUMBER: 41,198
REFERENCE/WORK ORDER NUMBER: 2074 97036
TELECOMMUNICATION INFORMATION:
TELEPHONE: 412-471-8815
TELEFAX: 412-471-4094
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1272 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: coding sequence
LOCATION: 8...1111
OTHER INFORMATION:

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: INFORMATION FOR SEQ ID NO: 96:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 34063
:   TYPE: nucleic acid
:   STRANDEDNESS: double
:   TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-09-454-7028-96

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Query Match: 2.88; Score 17; Eb 4; Length 34063;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 198 ATAAATCAACCACTG 214
    |||||
Db 42443 ATAAATCAACCACTG 32345

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Search completed: November 8, 2002, 06:10:45
 Job Time : 42.4146 secs

FEATURES

SOURCE

Location/Qualifiers

1. 707

/organism "Entamoeba histolytica"

/strain "M1-1985"

/db "M1-1985"

/feature "Entamoeba histolytica Sheared DNA"

/note "Vector: pUC19. Site: Not constructed at the Institute for Genome Research (IGR), Rockville, MD."

genomic DNA isolated from both cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.O., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. EXP. Parasitol. 77:450). The DNA was mechanically sheared to give a

fragment size distribution of 2-5 kb. The DNA was then used for the library construction as described in detail in Smith, H.O., and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing. Projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Bartell, Oxford University Press, 1999)."

BASE COUNT

419 a

122 c

120 g

346 t

ORIGIN

Query Match

Best Local Similarity 100.0% Prod. No. 15

Matches 22 Conservative 0 Mismatches 0 Indels 0 Gaps 0

ID

461 ATTTCAGACAGAAATGCTTTT 482

11111111111111111111

758

RESULT 2

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

LOCALIZATION/QUALIFIERS

1. 503

/organism "Sus scrofa"

/strain "crossbred"

/db "M1-P-E4-ABE-0-09-1-UM"

/feature "M1-P-E4-ABE-0-09-1-UM"

/note "M1-P-E4-ABE-0-09-1-UM"

/db "M1-P-E4-ABE-0-09-1-UM"

/feature "M1-P-E4-ABE-0-09-1-UM"

/note "M1-P-E4-ABE-0-09-1-UM"

/db "M1-P-E4-ABE-0-09-1-UM"

/feature "M1-P-E4-ABE-0-09-1-UM"

/note "M1-P-E4-ABE-0-09-1-UM"

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/note "M1-P-E4-ABE-0-09-1-UM"

polyclonal library. Not a Site 2. Probe: The M1-P-E4 library is derived from embryo at gestational day 14. For a detailed description of the library from which this clone was derived, please visit our web site at <http://www.igrr.edu/entamoeba/igrr/igrr.html>

IGR LIB M1-P-E4

IGR TISSUE Postconception_d_14.conceptus

IGR_SEQ ATTCAC

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Fri Nov 8 12:51:23 2002

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Page 8

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

RUN ON: November 7, 2002, 08:51:15 : Search time 1730.36 Seconds
(with about 300 records)

10259-668 Million cell updates/500

Title:	US-09-755-633-4
Portfolio score:	610

Sequence: 1 CAGGCTGGAGTGTATTTTCCTCCTGCAATATATLTAAG 610

Gapor 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Listing first 45 summaries

Database

1:	qb_bar:
2:	qb_hlg:
3:	qb_in:
4:	qb_on:
5:	qb_ov:
6:	qb_pat:
7:	qb_ph:
8:	qb_pl:
9:	qb_pre:
10:	qb_ro:
11:	qb_srs:
12:	te_57:
13:	qb_un:
14:	qb_v1:
15:	em_bar:
16:	em_bum:
17:	em_hum:
18:	em_inv:
19:	em_mi:
20:	em_om:
21:	em_or:
22:	em_ort:
23:	em_pat:
24:	em_ph:
25:	em_pl:
26:	em_ro:
27:	em_srs:
28:	em_un:
29:	em_v1:
30:	em_bum:
31:	em_hum:
32:	em_hc_other:
33:	em_hu_mis:
34:	em_hu_pln:
35:	em_hu_rpd:
36:	em_hu_mam:
37:	em_hu_vft:
38:	em_sy:
39:	em_hto_hum:
40:	em_hu_omis:
41:	em_hu_others:

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the
and is derived by adding score to the total score of

SUMMARY

Result	No.	Score	Query	Match	Length	Ref.	ID
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	2	405.8	65.5	405	1	AX+25446	
	3	401.8	65.9	405	1	AX+08346	
	4	379	62.1	379	1	ES1+39	
	5	379	62.1	379	1	ES1+91	
	6	374	62.1	374	1	MS1+5K	
	7	377.4	61.9	374	1	ES1+171A	
	8	364.4	59.7	258	4	AX+5538	
	9	357.4	58.6	529	4	NS+134452	
	10	341	55.9	405	4	AF+8770	
	11	337.8	55.4	406	4	EDU+1947	
	12	329.8	54.1	406	4	AFU+1138	
	13	329.8	54.1	405	4	UT+NTF005	
	14	326.6	53.5	405	4	NSP+100088	
	15	281.2	46.1	454	4	APR+1372	
	16	280.2	45.9	405	9	AF+34756	
	17	275.4	45.1	405	9	LEY+IN5A	
	18	273.8	44.9	405	9	MMU+19648	
	19	267.4	43.8	504	10	CY3434088	
	20	250	41.0	414	4	AX+43948	
	21	244.2	40.0	494	1	FEVRES	
	22	243.4	39.9	421	12	STML5A	
	23	232	38.0	470	4	A00+50	
	24	232	38.0	470	4	A00+50	
	25	221.6	36.3	448	10	AF+48211	
	26	221	36.2	194	10	PE+NT52	
	27	217.6	35.7	154	6	E01483	
	28	217.6	35.7	154	6	E17320	
	29	217.6	35.7	154	10	MLP5K	
	30	217.6	35.7	154	10	MLP5K	
	31	212.8	34.9	626	10	MSB0155A	
	32	209.6	34.4	481	6	10+462	
	33	207.4	34.0	429	6	AX+2138	
	34	207.4	34.0	429	6	AX+08095	
	35	206.4	33.8	429	6	E10+143	
	36	206.4	33.8	429	6	E17+19	
	37	202.6	32.9	429	6	EN+01399	
	38	181.4	29.7	429	6	AX+49761	
	39	178.6	29.2	429	6	AX+40763	
	40	172.2	28.2	429	6	AX+40766	
	41	171.8	27.6	429	6	AX+39420	
	42	168.6	27.6	429	6	AX+40765	
	43	166.4	27.3	429	6	AX+39247	
	44	166	27.3	411	6	AX+40771	
	45	163.4	26.8	411	6	AX+40769	

ACKNOWLEDGMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
AF331919	AF331919	Canis familiaris (dog) beta-5 globin	AF331919	AF331919.1	beta-5 globin	Canis familiaris	Canis familiaris	Eukaryota; Metazoa; Mammalia; Eutheria; Carnivora; Fissipedia 1 (bases 1 to 619)	Yano, S., Sekizawa, K., Watabe, T. and Mori	Canine interferon- γ molecular characterization and functional expression of a highly polymorphic gene

[illegible]

Query Match	46.18	Score 281.2	Dh 4	Length 554
Best Local Similarity	87.58	Prod. No. 6, 36-66		
Matches 407	Conservation 0	Mismatches 44	Indels 0	Gaps 0

[illegible]

Search completed: November 7, 2002, 16:43:10
Job time : 1745.46 secs

[illegible]

RES11.1 5
AA174300
11) AA174300 standard; DNA; 405 bp.

01	04 MAY-2001 (first entry)
XX	
1F	codine interleukin-5 coding sequence #1
XX	

Interleukin-5; IL-5; allergy; asthma; gene therapy;
inflammatory reaction; ds.

OS	caus sp.
XX	
PN	W020011049-AZ.
XX	
PD	15-FEB-2001

PE	09-AUG-2000; 2000WC-US21651
XX	
PR	10-AUG-1999; 99US-0371615

17A (11)XXX 17A11 INC.

PI Cho H, Lawton R, Mermet B, Alayolga A, XX

DOI: 10.1002/anie.200902615

Index

XX
XX

1. $\frac{1}{2}$ 2. $\frac{1}{3}$ 3. $\frac{1}{4}$ 4. $\frac{1}{5}$ 5. $\frac{1}{6}$ 6. $\frac{1}{7}$ 7. $\frac{1}{8}$ 8. $\frac{1}{9}$ 9. $\frac{1}{10}$ 10. $\frac{1}{11}$ 11. $\frac{1}{12}$ 12. $\frac{1}{13}$ 13. $\frac{1}{14}$ 14. $\frac{1}{15}$ 15. $\frac{1}{16}$ 16. $\frac{1}{17}$ 17. $\frac{1}{18}$ 18. $\frac{1}{19}$ 19. $\frac{1}{20}$ 20. $\frac{1}{21}$ 21. $\frac{1}{22}$ 22. $\frac{1}{23}$ 23. $\frac{1}{24}$ 24. $\frac{1}{25}$ 25. $\frac{1}{26}$ 26. $\frac{1}{27}$ 27. $\frac{1}{28}$ 28. $\frac{1}{29}$ 29. $\frac{1}{30}$ 30. $\frac{1}{31}$ 31. $\frac{1}{32}$ 32. $\frac{1}{33}$ 33. $\frac{1}{34}$ 34. $\frac{1}{35}$ 35. $\frac{1}{36}$ 36. $\frac{1}{37}$ 37. $\frac{1}{38}$ 38. $\frac{1}{39}$ 39. $\frac{1}{40}$ 40. $\frac{1}{41}$ 41. $\frac{1}{42}$ 42. $\frac{1}{43}$ 43. $\frac{1}{44}$ 44. $\frac{1}{45}$ 45. $\frac{1}{46}$ 46. $\frac{1}{47}$ 47. $\frac{1}{48}$ 48. $\frac{1}{49}$ 49. $\frac{1}{50}$ 50. $\frac{1}{51}$ 51. $\frac{1}{52}$ 52. $\frac{1}{53}$ 53. $\frac{1}{54}$ 54. $\frac{1}{55}$ 55. $\frac{1}{56}$ 56. $\frac{1}{57}$ 57. $\frac{1}{58}$ 58. $\frac{1}{59}$ 59. $\frac{1}{60}$ 60. $\frac{1}{61}$ 61. $\frac{1}{62}$ 62. $\frac{1}{63}$ 63. $\frac{1}{64}$ 64. $\frac{1}{65}$ 65. $\frac{1}{66}$ 66. $\frac{1}{67}$ 67. $\frac{1}{68}$ 68. $\frac{1}{69}$ 69. $\frac{1}{70}$ 70. $\frac{1}{71}$ 71. $\frac{1}{72}$ 72. $\frac{1}{73}$ 73. $\frac{1}{74}$ 74. $\frac{1}{75}$ 75. $\frac{1}{76}$ 76. $\frac{1}{77}$ 77. $\frac{1}{78}$ 78. $\frac{1}{79}$ 79. $\frac{1}{80}$ 80. $\frac{1}{81}$ 81. $\frac{1}{82}$ 82. $\frac{1}{83}$ 83. $\frac{1}{84}$ 84. $\frac{1}{85}$ 85. $\frac{1}{86}$ 86. $\frac{1}{87}$ 87. $\frac{1}{88}$ 88. $\frac{1}{89}$ 89. $\frac{1}{90}$ 90. $\frac{1}{91}$ 91. $\frac{1}{92}$ 92. $\frac{1}{93}$ 93. $\frac{1}{94}$ 94. $\frac{1}{95}$ 95. $\frac{1}{96}$ 96. $\frac{1}{97}$ 97. $\frac{1}{98}$ 98. $\frac{1}{99}$ 99. $\frac{1}{100}$ 100. $\frac{1}{101}$ 101. $\frac{1}{102}$ 102. $\frac{1}{103}$ 103. $\frac{1}{104}$ 104. $\frac{1}{105}$ 105. $\frac{1}{106}$ 106. $\frac{1}{107}$ 107. $\frac{1}{108}$ 108. $\frac{1}{109}$ 109. $\frac{1}{110}$ 110. $\frac{1}{111}$ 111. $\frac{1}{112}$ 112. $\frac{1}{113}$ 113. $\frac{1}{114}$ 114. $\frac{1}{115}$ 115. $\frac{1}{116}$ 116. $\frac{1}{117}$ 117. $\frac{1}{118}$ 118. $\frac{1}{119}$ 119. $\frac{1}{120}$ 120. $\frac{1}{121}$ 121. $\frac{1}{122}$ 122. $\frac{1}{123}$ 123. $\frac{1}{124}$ 124. $\frac{1}{125}$ 125. $\frac{1}{126}$ 126. $\frac{1}{127}$ 127. $\frac{1}{128}$ 128. $\frac{1}{129}$ 129. $\frac{1}{130}$ 130. $\frac{1}{131}$ 131. $\frac{1}{132}$ 132. $\frac{1}{133}$ 133. $\frac{1}{134}$ 134. $\frac{1}{135}$ 135. $\frac{1}{136}$ 136. $\frac{1}{137}$ 137. $\frac{1}{138}$ 138. $\frac{1}{139}$ 139. $\frac{1}{140}$ 140. $\frac{1}{141}$ 141. $\frac{1}{142}$ 142. $\frac{1}{143}$ 143. $\frac{1}{144}$ 144. $\frac{1}{145}$ 145. $\frac{1}{146}$ 146. $\frac{1}{147}$ 147. $\frac{1}{148}$ 148. $\frac{1}{149}$ 149. $\frac{1}{150}$ 150. $\frac{1}{151}$ 151. $\frac{1}{152}$ 152. $\frac{1}{153}$ 153. $\frac{1}{154}$ 154. $\frac{1}{155}$ 155. $\frac{1}{156}$ 156. $\frac{1}{157}$ 157. $\frac{1}{158}$ 158. $\frac{1}{159}$ 159. $\frac{1}{160}$ 160. $\frac{1}{161}$ 161. $\frac{1}{162}$ 162. $\frac{1}{163}$ 163. $\frac{1}{164}$ 164. $\frac{1}{165}$ 165. $\frac{1}{166}$ 166. $\frac{1}{167}$ 167. $\frac{1}{168}$ 168. $\frac{1}{169}$ 169. $\frac{1}{170}$ 170. $\frac{1}{171}$ 171. $\frac{1}{172}$ 172. $\frac{1}{173}$ 173. $\frac{1}{174}$ 174. $\frac{1}{175}$ 175. $\frac{1}{176}$ 176. $\frac{1}{177}$ 177. $\frac{1}{178}$ 178. $\frac{1}{179}$ 179. $\frac{1}{180}$ 180. $\frac{1}{181}$ 181. $\frac{1}{182}$ 182. $\frac{1}{183}$ 183. $\frac{1}{184}$ 184. $\frac{1}{185}$ 185. $\frac{1}{186}$ 186. $\frac{1}{187}$ 187. $\frac{1}{188}$ 188. $\frac{1}{189}$ 189. $\frac{1}{190}$ 190. $\frac{1}{191}$ 191. $\frac{1}{192}$ 192. $\frac{1}{193}$ 193. $\frac{1}{194}$ 194. $\frac{1}{195}$ 195. $\frac{1}{196}$ 196. $\frac{1}{197}$ 197. $\frac{1}{198}$ 198. $\frac{1}{199}$ 199. $\frac{1}{200}$ 200. $\frac{1}{201}$ 201. $\frac{1}{202}$ 202. $\frac{1}{203}$ 203. $\frac{1}{204}$ 204. $\frac{1}{205}$ 205. $\frac{1}{206}$ 206. $\frac{1}{207}$ 207. $\frac{1}{208}$ 208. $\frac{1}{209}$ 209. $\frac{1}{210}$ 210. $\frac{1}{211}$ 211. $\frac{1}{212}$ 212. $\frac{1}{213}$ 213. $\frac{1}{214}$ 214. $\frac{1}{215}$ 215. $\frac{1}{216}$ 216. $\frac{1}{217}$ 217. $\frac{1}{218}$ 218. $\frac{1}{219}$ 219. $\frac{1}{220}$ 220. $\frac{1}{221}$ 221. $\frac{1}{222}$ 222. $\frac{1}{223}$ 223. $\frac{1}{224}$ 224. $\frac{1}{225}$ 225. $\frac{1}{226}$ 226. $\frac{1}{227}$ 227. $\frac{1}{228}$ 228. $\frac{1}{229}$ 229. $\frac{1}{230}$ 230. $\frac{1}{231}$ 231. $\frac{1}{232}$ 232. $\frac{1}{233}$ 233. $\frac{1}{234}$ 234. $\frac{1}{235}$ 235. $\frac{1}{236}$ 236. $\frac{1}{237}$ 237. $\frac{1}{238}$ 238. $\frac{1}{239}$ 239. $\frac{1}{240}$ 240.

The present invention provides the protection and coding sequences of the various information-carrying regions of a nucleic acid molecule.

(c) Cancer and inflammatory reactions in dogs. The present sequence is one of the first of a series of studies in the laboratory of the author.

XX
Sedimento 405 BP: 131 A: 77 C: 44 G: 104 F: 0 other:

Query Match: 65.98; Score 401.8; DB 22; Length 405

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90	100	0	0	0

29 ATTACCAATGCTTCTGAATTGGCTTTGCTTAACTCTTGGGCTGGCTATGCTTCTGGCTTT 88

[illegible]

RESULT 7
AAF20979

AC: AAF-2(1)9799-

14-MAR-2011 04:15:01

Human flow-adaptation to a 1000-m/s² acceleration

KM Low adenosine and isovase concentrations may indicate low levels of

KM Immunosuppressive drugs inhibit the development of

respiratory obstructive pulmonary obstructive
surfactant hypoproductive pulmonary vascular
KM

KW pulmonary hypertension; congestive pulmonary; left

Canoe; ss.
KW

OS Homo sapien

W0200062746-A2.

26-(X) 2000-

Abstract

XX	1999	9.91%
XX	1999	9.91%

PA (NYCH/), NYCH J W.

NY 66-1571

2000-2001

low adenosine (A) content and high G/C content.

PT 'cancers and respiratory obstructions -
 YX

XX
 Disclosure; Page 788; 11/24/11; Final Issue

CC - No present inventory in stock; low addition to ΔV .

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QY	35	ATGCTTCGAAATTTGATTTGCTTACTTCTTGGAGTGGCTATATTTCTGGCTTGGCTGA	94							
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QY	95	GAAGATTCGATGAATTAAGCTGGTGGGAGAGAGCTTGAACCTGGCTGACATGACGAGCT	154							
DB	61	GAAGATTCGATGAATTAAGCTGGTGGGAGAGAGCTTGAACCTGGCTGACATGACGAGCT	120							
QY	155	TGGCTGATAGGCGAATGGAACTGATGATCTTCTACTGCTGAAATATAAAAATCAGCACTG	214							
DB	121	CTGGCTGATAGGCGAATGGAACTGATGATCTTCTACTGCTGAAATATAAAAATCAGCACTG	180							
QY	215	TGCATTAATGACATTTTCAAGATATAGATACATTTGAAATACGCAAGCTGGGAGGAGAG	274							
DB	181	TGCATTAATGACATTTTCAAGATATAGATACATTTGAAATACGCAAGCTGGGAGGAGAG	240							
QY	275	GCTGTGGATTAAGCTATTCGCAAAACTTGTCTTAAATAAAGACACATAGAGGCCCAAAA	334							
DB	241	GCTGTGGATTAAGCTATTCGCAAAACTTGTCTTAAATAAAGACACATAGAGGCCCAAAA	300							
QY	335	AAAGAGCTGTATAGAGGAAAGATGAGAGATGAATAAGTTCTTAACTACTGCAAGTATTT	394							
DB	301	AAAGAGCTGTATAGAGGAAAGATGAGAGATGAATAAGTTCTTAACTACTGCAAGTATTT	360							
QY	495	CTTGTATTAATAAAGACAGCTGGATACGCGGAAAGTGA	433							
DB	461	CTTGTATTAATAAAGACAGCTGGATACGCGGAAAGTGA	399							

Search completed: November 6, 2002, 11:17:35
Job time : 168.274 secs


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544640-1
Patent No. 5,424,440
APPLICANT: Human, Tasugeto, Robert, Kiyoshi, Soren, Peter, Etc.
TITLE OF INVENTION: HUMAN B CELL DIFFERENTIATION FACTOR AND
PROCESS OF PRODUCING SAID FACTOR
NUMBER OF SEQUENCES: 2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09-755-633
FILING DATE: 21 SEP 1987
SHO ID NO: 1
LENGTH: 4240

Query Match: 25.0% Score 152.4; DB 6, Length 4240,
Host Local Similarity 77.3%; Prod. No. 5,20-48;
Matches 192; Conservative 0; Mismatches 56; Indels 0; Gaps 1.

QY 431 AAAAAAAGTGTGAGAGAAATATGAGAGAGAGAAATTTGTGACTACTGTAAAT 390
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
DB 2114 ACAAAGAAAGTGTGAGAGAAATATGAGAGAGAGAAATTTGTGACTACTGTAAAT 2173

QY 431 ATTCTTGCTATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 450
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
DB 2174 GTTCTTGCTATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2233

QY 451 GTAGTGAAATTTTGAGAGAAATG--GTTTGTGAGAGAGAGAGAGAGAGAGAGAGAG 509
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DB 2244 GCAAGTAAATTTTGAGAGAAATG--GTTTGTGAGAGAGAGAGAGAGAGAGAGAGAG 2293

QY 509 GAGTAAAGTATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 568
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DB 2294 GAGTAAAGTATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2353

QY 569 TCTACTACTATTATCA 584
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
DB 2454 TACTACTACTATTATCA 2369

RESULT 7
US-09-629-644A-5
Sequence 5, Application US/0862964A
Patent No. 6,025,499
GENERAL INFORMATION:
APPLICANT: Lee, J. L.
APPLICANT: Lee, N. A.
TITLE OF INVENTION: 11-5 TRANSGENIC MOUSE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Schweigert, Lindbergh, Wessner & Kintz, P. A.
STREET: P. O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09-629,643A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/624,643
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viksins, Ann S.
REGISTRATION NUMBER: 37,748
REFERENCE/WORKSHEET NUMBER: 150,167W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-359-3260
TELEFAX: 612-359-3263

```

```

INFORMATION FOR SHO ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 6727 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURES:
NAME/KEY: put_leptide
LOCATION: 650..3771
OTHER INFORMATION: Join 650..710, 1560..1592,
OTHER INFORMATION: 3468..3596, 3676..3771
US-09-629-643A-5

Query Match: 14.9% Score 90.6; DB 6, Length 6727;
Host Local Similarity 76.6%; Prod. No. 1,80-18;
Matches 111; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 204 ATCAATACATCTGCATTAAGAAATTTTTCAGAGTATAAGAAATTCAGAAATCAATG 263
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DB 4466 AGCAATACATCTGCATTAAGAAATTTTTCAGAGTATAAGAAATTCAGAAATCAATG 3525

QY 264 GCGACGCGGAGGCTGTGGATTAATTAATGCAAAATTTGCTTAATTAATAATGACATAG 323
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
DB 3526 TCGGTGAGGAGATGTGGAAATGATATTCAGAAATTCAGAAATTCAGAAATCAATG 3585

QY 324 AGCGCAAAAAAAGGTGTGAG 348
+ + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + + +
DB 3586 AGCGTAAAAAGTTCGAGAG 3610

RESULT 9
US-09-155-884-5
Sequence 5, Application US/09155884

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1 Patent No. 6215040
2
3 GENERAL INFORMATION:
4 APPLICANT: James J. Lee et al.
5 TITLE OF INVENTION: IL-5 TRANSGENIC MOUSE
6 NUMBER OF SEQUENCES: 5
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Schweppes, Lundberg, Weesner & Kluth, P. A.
9 STREET: P. O. Box 2938
10 CITY: Minneapolis
11 STATE: MN
12 COUNTRY: USA
13 ZIP: 55402
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Diskette
17 COMPUTER: IBM compatible
18 OPERATING SYSTEM: DOS
19 SOFTWARE: FASTSEQ Version 2.0
20
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/155,884
23 FILING DATE: Unknown
24 CLASSIFICATION:
25
26 FOR APPLICATION DATA
27 APPLICATION NUMBER: PCT/US97/05932
28 FILING DATE: 09-APR-1997
29 ATTORNEY/AGENT: SCHERRA, JEN
30 NAME: VIRSHUP, Ann S.
31 REGISTRATION NUMBER: 37,748
32 REFERENCE/EXCERPT NUMBER: 150,167982
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 612-359-3260
35 TELEFAX: 612-319-3061
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BASE COUNT 375 a 115 c 146 g 164 t 105 others
 ORIGIN

Query Match 6.4% Score 39.2; DB 17; Length 905;

Best Local Similarity 42.0%; Prod. No. 11;
 Matches 74; Conservative 22; Mismatches 80; Indels 0; Gaps 0;

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 DB 324 GAAAAAAAAAAAAAAAAATWAAAAAAAAAAACWCTTGAAGWATTAAMRAAMAAA 383
 QY 254 AACTAACTGCTCACTGAGCTGTGATTAACATATCCAAACTTGTCTTAATAAAA 313
 DB 384 AAAAAATWCAACCAAAWMTWAAAAWMTWAAAAWMTWAAAAAGTGTCTTWAAAAAAR 443
 QY 314 GAATCATATACCTGCAAAAAAAGCTGTGAGAGCAAGCATGAGAGTGAACAA 369
 DB 444 MARGWTGCAAAAAAGCAAAAAAAGTAAAAAGCGGGAAMRGGGGTATATAAAA 499

Search completed: November 7, 2002, 11:57:53
 Job time: 1137.47 secs



GenCore version 5.1.3
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OM nucleotide search, using sw model

Run on: November 7, 2002, 08:51:15, Search time 1'30:26 Seconds

(without alignments)
10268168 Million cell updates/sec

Title: US-09-755-633-6

Perfect score: 610

Sequence: 1 ctcaataataattcattcattggt.....aattctcagtg ttgctctg 610

Scoring table: 0.130_NUC
Gapop 60.0, Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 0

Total number of hits satisfying chosen parameters: 410+260

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: GenEmbl:

- 1: qb_dai:*
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- 39: qb_dai:*
- 40: qb_dai:*
- 41: qb_dai:*

Score greater than or equal to the score of the
and is derived by analysis of the total score

SUMMARIES

Result No.	Score	Query Match	Length	HL
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3	271	44.4	400	4
4	250	41.0	400	4
5	170	27.9	160	4
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7	43	7.0	1140	4
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42	21	3.4	400	4
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45	21	3.4	400	4

ALIGNMENTS

RESULT 1	AF331919	610 bp	RNA
LOCUS	Canis familiaris		
DEFINITION	Canis familiaris		
ACCESSION	AF331919		
VERSION	AF331919.1		
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			



WP1: 2000-0724/23/06.
P-PSDB: AAV58219.

Nucleic acids encoding immunoregulatory proteins from cats or dogs,
useful for treating or preventing e.g. tumors or autoimmune disease

Claim 1b: Page 223-224; 264pp; English.

Sequences AA25546-25551 represent cDNA sequences encoding
canine interleukin-5 (IL-5). The invention relates to canine
IL-4, canine or feline IL-3 ligand, canine or feline CD40, canine or
feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
interferon-alpha (IFN-alpha) and feline granulocyte macrophage
colony-stimulating factor (GM-CSF), and nucleotides which encode these
immunoregulatory proteins. The proteins, their associated
nucleic acids, specific antibodies and inhibitors may be used as
vaccines for therapeutic or prophylactic regulation of an immune
response in animals (particularly cats, dogs, horses and humans).
They may be used to treat autoimmune or infectious diseases including
allergies, tumors, inflammation and graft rejection, and to increase
the response from a co-administered antigen. The nucleotide sequences
can also be used for the recombinant production of a protein, while
as sources of inhibitory therapeutics (e.g., antisense
oligonucleotides). The proteins may be used to raise antibodies and to
screen for modulators of activity, while the antibodies may be used in
detection, and in drug targeting.

Sequence 610 BP; 202 A; 114 G; 139 G; 155 T; 0 other;

Query Match: 100.0%; Score 610; DB 21; Length 610;
Best Local Similarity: 100.0%; Pred. No. 2,30-307;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CTCGAATATATTCATCTGTCGAGAGTAAATAGAGAGCCGGAATATTACTT 60
DB 610 CTCGAATATATTCATCTGTCGAGAGTAAATAGAGAGCCGGAATATTACTT 60
QY 61 TCTCTCTAGCTTACTATATAGTAAATAGAGAGCCGGAATATTACTT 120
DB 550 TCTCTCTAGCTTACTATATAGTAAATAGAGAGCCGGAATATTACTT 120
QY 121 CATGCGCAAAAACGATCTCTGTCGAGAGTAAATAGAGAGCCGGAATATTACTT 180
DB 490 CATGCGCAAAAACGATCTCTGTCGAGAGTAAATAGAGAGCCGGAATATTACTT 180
QY 181 ACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 430 ACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 CTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB 379 CTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 301 TATTAAACAGAGTTTGGAGTATGATGATGATGATGATGATGATGATGATGATG 360
DB 310 TATTAAACAGAGTTTGGAGTATGATGATGATGATGATGATGATGATGATGATG 360
QY 361 CAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
DB 250 CAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
QY 421 AGTAGAGATCAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
DB 190 AGTAGAGATCAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
QY 481 CAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
DB 130 CAAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
QY 541 ATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
DB 70 ATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600

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QY 601 GTTTCCTTG 610

DB 10 GTTTCCTTG 1

AA25547 standard; cDNA: 610 BP.

11-MAR 2000 (first entry)

Canine interleukin-5 (IL-5) cDNA complement.

Interleukin-5, IL-5, antibody, canine, inhibitor, immune response,
immunoregulation, tumour, cancer, autoimmune disease, vaccine, etc.
Cancer, familialis.

Key: Location/Qualifiers
FT Complement (178..582)
FT /tag= a
FT /product= "Canine IL-5"

W09961618-A2.

02-DEC-1999.

28-MAY-1999; 99WO-0511942.

29-MAY-1998; 98US-0087306.

(HESKA) HESKA CORP.

Sim G, Yang S, Dreitz MJ, Wonderling RS;

WP1: 2000-0724/23/06.

P-PSDB: AAV58219.

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useful for treating or preventing e.g. tumors or autoimmune disease

Claim 1b: Page 223-225; 264pp; English.

Sequences AA25546-25551 represent cDNA sequences encoding
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IL-4, canine or feline IL-3 ligand, canine or feline CD40, canine or
feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
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colony-stimulating factor (GM-CSF), and nucleotides which encode these
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vaccines for therapeutic or prophylactic regulation of an immune
response in animals (particularly cats, dogs, horses and humans).
They may be used to treat autoimmune or infectious diseases including
allergies, tumors, inflammation and graft rejection, and to increase
the response from a co-administered antigen. The nucleotide sequences
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screen for modulators of activity, while the antibodies may be used in
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Sequence 610 BP; 155 A; 139 G; 114 G; 202 T; 0 other;

Query Match: 100.0%; Score 610; DB 21; Length 610;
Best Local Similarity: 100.0%; Pred. No. 2,30-307;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTCGAATATATTCATCTGTCGAGAGTAAATAGAGAGCCGGAATATTACTT 60


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Db 252 CAAAGCTCTCCGCGGGGACGTTGGTTCTCAATCTGTCATACCCGCAAAACTCTCTT 193
Gy 491 AATGACAGTGGTGGTTATTTTTCAGACATAGACATGACACCTGCAACGGCTAT 450
Db 132 AATGACAGTGGTGGTTATTTTTCAGACATAGACATGACACCTGCAACGGCTAT 133
Gy 451 CAAACAAATTCGATGAGTGAACAGACAGTGTGCTGACAGCTGATATCATGGA 510
Db 132 CAGCGCAATTCGATGAGTGAACAGACAGTGTGCTGACAGCTGATATCATGGA 73
Gy 511 ATTTTCATGACAGCAAGGACATGAATATAGACAGCCCTCAGAGCTAGCAAAATCAATTCAG 570
Db 72 ATTTTCATGACAGCAAGGACATGAATATAGACAGCCCTCAGAGCTAGCAAAATCAATTCAG 13
Gy 571 AAGCATTCCTCAT 582
Db 12 AAGCATTCCTCAT 1

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RESULT 10

AA150756/c
ID AA150756 standard; cDNA; 499 bp.

AC AA150756;

DI 24-SEP-1997 (first entry)

DE ovine IL-5 cDNA.

XX Cytokine: ovine sheep interleukin 5; interleukin-12; IL-5; IL-12;

KW livestock; ovine stress; transport; vaccine; adjuvant; interferon;

KW cancer; immunosuppression; allergy; reproductive system; growth;

KW early maturity; antibody; diagnosis; immunopotentiator;

KW early hematopoietic production; cell; cytokine; cell; lymphocyte;

KW secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss;

XX Ovis ammon aries.

XX W09700421-A1.

XX 03-JAN-1997.

XX 14-JUN-1996; 96WO-AU00360.

XX 27-OCT-1995; 95AU-0006244.

XX 14-JUN-1995; 95AU-0003502.

XX (CSIR) OMMNMEALFH SFT & INP RES 0803.

XX Siew H, Wood P;

XX WPI; 1997 077528/07.

XX P-PSDB; AAM08479.

XX Nucleic acid encoding ovine interleukin-5 or -12 used as vaccine

XX adjuvants and to treat or prevent microbial infections in livestock

XX claim 6; Page 41-42; 78pp; English.

XX The sequence 11256 to AA150755 56 encode ovine interleukin-5 (IL-5).

XX Ovine IL-5 or IL-12 are used to treat and/or prevent infections in

XX livestock (cows and sheep); particularly where the animals are

XX stressed; e.g. during transport. IL-5 and IL-12 can also be used as

XX adjuvants in vaccines for veterinary use (partic. weakly immunogeni-

XX c subunit of synthetic peptide vaccines). They may also be used to

XX treat cancer (immunosuppression and thereby to enhance/suppress the

XX reproductive system and to promote growth or early maturity). Additionally

XX antibodies can be delivered from constructs of delivery cells and

XX antibodies are useful in enzyme immunoassays for rapid diagnosis of

XX infection. The interleukins are immunopotentiators, especially IL-5,

XX promotes growth of early hematopoietic progenitor cells and generation

XX of cytotoxic cells from thymocytes, also to stimulate production and

CC secretion of IgM and IgG (in synergism with both

CC IL-12 induces production of gamma-interferon by

CC of T and NK cells and induces the (non-28000

CC lymphocyte response; the non-28000 construct and

CC in vitro production of IL-5 or IL-12.

XX Sequence 499 bp; 13 Amino acids; 99 13 13

SO Query Match

Query Match

Best local similarity: 100.00; proc. No. 470-123

Matches 43; Conservative 0; Mismatches 0

Gy 457 CTAACAGCTGCTGAGTGAACATATAGACAGCCCTCAGAGCTAGCAAAATCAATTCAG 570

Db 110 CTAACAGCTGCTGAGTGAACATATAGACAGCCCTCAGAGCTAGCAAAATCAATTCAG 570

RESULT 11

AA150755/c

ID AA150755 standard; cDNA; 499 bp.

AC AA150755;

DI 24-SEP-1997 (first entry)

DE ovine IL-5 gene.

XX Cytokine: ovine sheep interleukin 5; interleukin-12; IL-5; IL-12;

KW livestock; ovine stress; transport; vaccine; adjuvant; interferon;

KW cancer; immunosuppression; allergy; reproductive system; growth;

KW early maturity; antibody; diagnosis; immunopotentiator;

KW early hematopoietic production; cell; cytokine; cell; lymphocyte;

KW secretion; IgM; IgA; bacterial endotoxin; gamma-interferon; ss;

XX Ovis ammon aries.

XX W09700421-A1.

XX 03-JAN-1997.

XX 14-JUN-1996; 96WO-AU00360.

XX 27-OCT-1995; 95AU-0006244.

XX 14-JUN-1995; 95AU-0003502.

XX (CSIR) OMMNMEALFH SFT & INP RES 0803.

XX Siew H, Wood P;

XX WPI; 1997 077528/07.

XX P-PSDB; AAM08479.

XX Nucleic acid encoding ovine interleukin-5 or -12 used as vaccine

XX adjuvants and to treat or prevent microbial infections in livestock

XX claim 6; Page 39-40; 78pp; English.

XX The sequence 11256 to AA150755 56 encode ovine interleukin-5 (IL-5).

XX Ovine IL-5 or IL-12 are used to treat and/or prevent infections in

XX livestock (cows and sheep); particularly where the animals are

XX stressed; e.g. during transport. IL-5 and IL-12 can also be used as

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XX c subunit of synthetic peptide vaccines). They may also be used to

XX treat cancer (immunosuppression and thereby to enhance/suppress the

XX reproductive system and to promote growth or early maturity). Additionally

XX antibodies can be delivered from constructs of delivery cells and

XX antibodies are useful in enzyme immunoassays for rapid diagnosis of

XX infection. The interleukins are immunopotentiators, especially IL-5,

XX promotes growth of early hematopoietic progenitor cells and generation

XX of cytotoxic cells from thymocytes, also to stimulate production and

Fri Nov 8 12:51:29 2002

us-09-755-633-6.rng

Page 10

Search completed: November 7, 2002, 22:02:41
Job Time: 164.172 secs

1 APPLICANT: HASTINGS, Stan
 2 APPLICANT: HEY, Allan W
 3 FILE OF INVENTION: AN INTERLEUKIN 5 ANTAGONIST
 4 FILE REFERENCE: 99726
 5 CURRENT APPLICATION NUMBER: US/09/180,864
 6 CURRENT FILING DATE: 1999-04-12
 7 PRIOR APPLICATION NUMBER: 08/551,438
 8 PRIOR FILING DATE: 1994-07-28
 9 NUMBER OF SEQ ID NOS: 4
 10 SOFTWARE: Patent In Ver. 2.1
 11 SEQ ID NO: 1
 12 LENGTH: 477
 13 TYPE: DNA
 14 ORGANISM: nucleotide sequence encoding modified IL-5
 15 FEATURE:
 16 NAME/KEY: CDS
 17 LOCATION: (4)..(466)
 18 US-09-180,864-1

Query Match 3.48; Score 21; DB 4; Length 377;
 Best Local Similarity 100.0%; Prod. No. 0.34;
 Matches 21; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

09 393 TGACATGTCATGTTTAT 413
 106 154 TGACATGTCATGTTTAT 184

1 RESULT 7
 2 SEQ-08-10957-16
 3 Sequence 16, Application PG/US0410957
 4 GENERAL INFORMATION:
 5 APPLICANT: Goldstein, Harris; Kollmann, Tobias R.
 6 TITLE OF INVENTION: Immunodeficient Mouse Models of
 7 TITLE OF INVENTION: Pathogenesis of Human Disease and Efficacy and Toxicity of
 8 TITLE OF INVENTION: Disease Treatments
 9 NUMBER OF SEQUENCES: 28
 10 CORRESPONDENCE ADDRESS:
 11 ADDRESS: Law Office of Sherman and Shalloway
 12 STREET: 413 N. Washington Street
 13 CITY: Alexandria
 14 STATE: Virginia
 15 COUNTRY: USA
 16 ZIP: 22314
 17 COMPUTER RELEASABLE FORM:
 18 MEDIUM TYPE: Diskette, 5.25 inch, 360 KB Storage
 19 COMPUTER: IBM Clone, 8086 Turbo
 20 OPERATING SYSTEM: MS DOS 5.0
 21 SOFTWARE: Word Perfect, Version 5.1
 22 CURRENT APPLICATION DATA:
 23 APPLICATION NUMBER: PCT/US04/10957
 24 FILING DATE:
 25 CLASSIFICATION:
 26 ATTORNEY/AGENT INFORMATION:
 27 NAME: Richard A. Stouffer
 28 REGISTRATION NUMBER: 26,588
 29 REFERENCE/KEY NUMBER: 09/10957-11
 30 TELECOMMUNICATION INFORMATION:
 31 TELEPHONE: (703) 549-2284
 32 TELEFAX: (703) 846-0106
 33 INFORMATION FOR SEQ ID NO: 16:
 34 SEQUENCE CHARACTERISTICS:
 35 LENGTH: 29 nucleotides
 36 TYPE: nucleic acid
 37 STRANDEDNESS: single
 38 TOPOLOGY: linear
 39 Molecule Type: cDNA
 40 HYPOTHETICAL: no
 41 ORIGINAL SOURCE:
 42 ORGANISM: human
 43 FEATURE:
 44 NAME/KEY: 3' UTR
 45 PCT-0804-10957-16

Query Match 3.48; Score 21; DB 4; Length 377;
 Best Local Similarity 100.0%; Prod. No. 0.34;
 Matches 21; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

09 393 TGACATGTCATGTTTAT 413
 DB 1 TGACATGTCATGTTTAT 184

1 RESULT 8
 2 US-08-621,841-48/
 3 Sequence 48, Application US/08-621,841
 4 Patent No. 6096869
 5 GENERAL INFORMATION:
 6 APPLICANT: Stanley, Margaret A.
 7 TITLE OF INVENTION: REAGENT FOR PATHOGENESIS
 8 TITLE OF INVENTION: LESIONS
 9 NUMBER OF SEQUENCES: 58
 10 CORRESPONDENCE ADDRESS:
 11 ADDRESS: Philip Roth, Esq., Attorney at Law
 12 STREET: Four Embarcadero, Suite 440
 13 CITY: San Francisco
 14 STATE: California
 15 COUNTRY: United States
 16 ZIP: 94111
 17 COMPUTER RELEASABLE FORM:
 18 MEDIUM TYPE: Floppy Disk
 19 COMPUTER: IBM PC compatible
 20 OPERATING SYSTEM: MS-DOS/Windows
 21 SOFTWARE: Patent In Ver. 2.1
 22 CURRENT APPLICATION DATA:
 23 APPLICATION NUMBER: 08/764,184
 24 FILING DATE: 22-MAR-1999
 25 CLASSIFICATION: 514
 26 PRIOR APPLICATION DATA:
 27 APPLICATION NUMBER: 08/607,840
 28 FILING DATE: 22-MAR-1996
 29 ATTORNEY/AGENT INFORMATION:
 30 NAME: Drogot, Walter H.
 31 REGISTRATION NUMBER: 41,474
 32 REFERENCE/KEY NUMBER: 08/764,184
 33 TELECOMMUNICATION INFORMATION:
 34 TELEPHONE: (415) 761-1000
 35 TELEFAX: (415) 596-0244
 36 INFORMATION FOR SEQ ID NO: 48:
 37 SEQUENCE CHARACTERISTICS:
 38 LENGTH: 21 base pairs
 39 TYPE: nucleic acid
 40 STRANDEDNESS: single
 41 TOPOLOGY: linear
 42 HYPOTHETICAL: NO
 43 ANTI-SENSE: NO
 44 US-08-621-841-48
 45 Query Match 3.48; Score 21; DB 4; Length 377;
 46 Best Local Similarity 100.0%; Prod. No. 0.34;
 47 Matches 21; Conserved 0; Mismatches 0; Indels 0; Gaps 0;

09 396 ACATGATGATGTTTAT 413
 DB 21 ACATGATGATGTTTAT 4

1 RESULT 9
 2 US-08-466,852-1/
 3 Sequence 1, Application US/08-466,852
 4 Patent No. 5681936
 5 GENERAL INFORMATION:
 6 APPLICANT:
 7 TITLE OF INVENTION: A DNA SEQUENCE FOR THE
 8 TITLE OF INVENTION: HUMAN HBBN INTERFER

```

NUMBER OF SEQUENCES: 4
CORRESPONDENT ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065 0907
COMPUTER REMARKS FORM:
MEDIUM TYPE: Diskette, 4.5 In., 1.44B
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 09/466,852
FILING DATE:
CLASSIFICATION: 124
ATTORNEY'S FIRM: FRAAT &
NAME: FRAAT, FRAAT &
REGISTRATION NUMBER: 36,752
REFERENCE/EXCERPT NUMBER: 19711A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3199
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NOS: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 Bases
TYPE: nucleic acid
STRANDS: single
POLYMER: linear
MOLECULE TYPE: DNA (genomic)
US 09-466-852-1

Query Match: 2.8%, Score 17, Ins 4, Length 149;
Post Local Similarity: 100.0%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 550 AACTAAAGAAATCAAT 566
11111111111111111111
DA 49 AACTAAAGAAATCAAT 23

RESULT 10
US-09-428-111-666-7:
Sequence 666, Application US/09428111
Patent No. 6,662,434
GENERAL INFORMATION:
APPLICANT: Endoche, William O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Asker, Jon H.
APPLICANT: Butters, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catlin, Theodore J.
APPLICANT: Dotti, Adrian
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Mahoney, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HEMAR GINS AND GIN EXPRESSION
FILE REFERENCE: GDB-257 (US)
CURRENT APPLICATION NUMBER: US/09/428,111
PUBLICATION DATE: 1999-04-08
EARLIER APPLICATION NUMBER: 66/0989,801
PUBLICATION DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 666
LENGTH: 449
TYPE: DNA
ORGANISM: Homo sapiens
US 09-428-111-666-7

```

```

Query Match: 2.8%, Score 17, Ins 4, Length 149;
Post Local Similarity: 100.0%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 422 TACTTATGACACAGCCT 438
11111111111111111111
DB 208 TACTTATGACACAGCCT 192

RESULT 11
US-09-428-116-171-7:
Sequence 171, Application US/094280116A
Patent No. 6,344,427
GENERAL INFORMATION:
APPLICANT: Robinson, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 79-124, P. 176,995
CURRENT APPLICATION NUMBER: US/09/428,116A
PUBLICATION DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 171
LENGTH: 323
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: prolyl oligopeptidases
US-09-428-116-171-7

Query Match: 2.8%, Score 17, Ins 4, Length 845;
Post Local Similarity: 100.0%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 409 TTATTTTCAGCAGTAG 425
11111111111111111111
DB 697 TTATTTTCAGCAGTAG 681

RESULT 12
US-09-869-137-1:
Sequence 1, Application US/08869137
Patent No. 5,856,157
GENERAL INFORMATION:
APPLICANT: Schlegel, David
APPLICANT: Craig, Richard
APPLICANT: Medford, June L.
APPLICANT: Murrah, R.O.
APPLICANT: Cox-Foster, Diana L.
TITLE OF INVENTION: A No. 78561570 59 11.0 ANT Fatty
FILE REFERENCE: Acid desaturase and GATE therefor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Webb Law Firm
STREET: 700 Koppers Building, 416 Seventh Avenue
CITY: Pittsburgh
STATE: PA
COUNTRY: USA
ZIP: 15219 1818
COMPUTER REMARKS FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 56/35/64,137
FILING DATE:
CLASSIFICATION: 435
PUBLICATION DATE: 60/018,957
APPLICATION NUMBER: 60/018,957
PUBLICATION DATE: 04-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Johnson, Barbara E

```


REGISTRATION NUMBER: 41,198
 REFERENCE/DOCKET NUMBER: 2074 970766
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 412-471 8815
 TELEFAX: 412-471-4094
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1272 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURES:
 NAME/KEY: Coding Sequence
 LOCATION: 8...1111
 OTHER INFORMATION:
 US-08-869-147-1

Query Match 2.88; Score 17; DB 2; Length 1272;
 Best Local Similarity 100.0%; Prod. No. 34;
 Matches 17; Conservative 0; Mismatches 0; Gaps 0;

UY 440 CCGTCGGCCAGTTGGT 356
 |||
 DB 415 CCGTCGGCCAGTTGGT 431

RESULT 14
 US-09-418-448-42/c
 Sequence 32; Application US/09418448
 Patent No. 6,210,950
 GENERAL INFORMATION:
 APPLICANT: Johnson, William G.
 TITLE OF INVENTION: METHODS FOR DNA SING, PREVENTING, AND HEATING
 FILE REFERENCE: 601-1-057
 CURRENT APPLICATION NUMBER: US/09/418 448
 CURRENT FILING DATE: 1999 05 25
 NUMBER OF SEQ ID NOS: 46
 SOFTWARE: Patent In Vot. 2.0
 SEQ ID NO 42
 LENGTH: 1547
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-318-448-42

Query Match 2.88; Score 17; DB 4; Length 1547;
 Best Local Similarity 100.0%; Prod. No. 34;
 Matches 17; Conservative 0; Mismatches 0; Gaps 0;

UY 407 TTTTATTTTAAATTA 423
 |||
 DB 602 TTTTATTTTAAATTA 586

RESULT 14
 US-09-023-023-1/c
 Sequence 1; Application US/09024024
 Patent No. 6,121,018
 GENERAL INFORMATION:
 APPLICANT: Kristine Kay Kiley
 TITLE OF INVENTION: Interleukin-1 beta Convert Inhibitors like Apoptosis In
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESS: Smithline Research Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: PA
 COUNTRY: USA
 ZIP: 19406
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette

COMPUTER: IBM 700/114
 OPERATING SYSTEM: OS
 SOFTWARE: FASTA 1.4 with as Version 2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 127 07 0004
 FILING DATE: 12 Feb 1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 127 07 0004
 FILING DATE: 12 Feb 1998
 ATTORNEY/AGENT INFORMATION:
 NAME: BAO, WILLIAM
 REGISTRATION NUMBER: 41,44
 REFERENCE/DOCKET NUMBER: 2074 970766
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-1411
 TELEFAX: 610-270-1404
 TELEX:
 INFORMATION FOR SEQ ID NO 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2071 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-023-023-1

Query Match 2.88; Score 17; DB 2;
 Best Local Similarity 100.0%; Prod. No. 34;
 Matches 17; Conservative 0; Mismatches 0;

UY 403 CCGATTTTATTTTAA 439
 |||
 DB 1219 CCGATTTTATTTTAA 586

RESULT 15
 US-09-453-7928-96/c
 Sequence 36; Application US/09453723
 Patent No. 6,165,723
 GENERAL INFORMATION:
 APPLICANT: Biotechnology Resources, Inc.
 TITLE OF INVENTION: Methods for
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESS: Biotechnology Resources, Inc.
 STREET: 15015 E. 1st Avenue
 CITY: Aurora, CO
 STATE: CO
 COUNTRY: US
 ZIP: 80012
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 Inch, 1.44MB
 COMPUTER: IBM PS/2 Model 550
 SOFTWARE: FASTA 1.4 with as Version 2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 127 07 0004
 FILING DATE: 12 Feb 1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 127 07 0004
 FILING DATE: 12 Feb 1998
 ATTORNEY/AGENT INFORMATION:
 NAME: BAO, WILLIAM
 REGISTRATION NUMBER: 41,44
 REFERENCE/DOCKET NUMBER: 2074 970766
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-1411
 TELEFAX: 610-270-1404
 TELEX:

1 INFORMATION FOR SEQ ID NO: 96:
 2 SEQUENCE CHARACTERISTICS:
 3 LENGTH: 44063
 4 TYPE: nucleic acid
 5 STRANDEDNESS: double
 6 TOPOLOGY: linear
 7 MOLECULE TYPE: DNA (genomic)
 8 SEQUENCE DESCRIPTION: SEQ ID NO: 96:
 9 US-09-453-702R 96

Query Match 2.88; Score 17; 100.0%; Length 34063;
 Best local Similarity 100.0%; Ident. No. 42;
 Matches 17; conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 CAGTTGGATTTTAT 413
 |||||||
 DB 42449 CAGTTGGATTTTAT 32144

Search completed: November 8, 2002, 09:10:41
 Job time : 33.4146 secs

Genome version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

4M nucleotide - nucleotide search, using sw model

Run on: November 7, 2002, 16:52:17 ; Search time 1140.78 seconds
(without alignment)
8746.696 Million cell updates/sec

Title: US-09-755-633-6

Footest score: 610
Sequence: 1 ctccatattatctatcttatattatcttcttctt 610

Scoring tables: 01105_NMC
Gapop 60.0 , Gapext 60.0

Searchset: 16154066 seqs, 8097743376 residues

Word size: 0

Total number of hits satisfying chosen parameters: 42308142

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listed first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	22	4.6	907	17	BH130589
2	21	3.4	503	14	BQ598873
3	20	3.3	305	9	A1666365
4	20	3.3	440	6	A1666365
5	20	3.3	478	17	A0134641
6	20	4.3	493	17	BH056804

7	20	4.4	411	17	B1156087
8	20	3.4	411	17	B1156087
9	20	4.4	411	17	B1156087
10	20	4.4	411	17	B1156087
11	20	4.4	411	17	B1156087
12	20	4.4	411	17	B1156087
13	20	4.4	411	17	B1156087
14	20	4.4	411	17	B1156087
15	20	4.4	411	17	B1156087
16	20	4.4	411	17	B1156087
17	20	4.4	411	17	B1156087
18	20	4.4	411	17	B1156087
19	20	4.4	411	17	B1156087
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21	20	4.4	411	17	B1156087
22	20	4.4	411	17	B1156087
23	20	4.4	411	17	B1156087
24	20	4.4	411	17	B1156087
25	20	4.4	411	17	B1156087
26	20	4.4	411	17	B1156087
27	20	4.4	411	17	B1156087
28	20	4.4	411	17	B1156087
29	20	4.4	411	17	B1156087
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31	20	4.4	411	17	B1156087
32	20	4.4	411	17	B1156087
33	20	4.4	411	17	B1156087
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35	20	4.4	411	17	B1156087
36	20	4.4	411	17	B1156087
37	20	4.4	411	17	B1156087
38	20	4.4	411	17	B1156087
39	20	4.4	411	17	B1156087
40	20	4.4	411	17	B1156087
41	20	4.4	411	17	B1156087
42	20	4.4	411	17	B1156087
43	20	4.4	411	17	B1156087
44	20	4.4	411	17	B1156087
45	20	4.4	411	17	B1156087

ALIGNMENTS

RESULT 1:
BH130589/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
ATTIBIOS
TITLE
JOURNAL
COMMENT

BH130589 907 bp cDNA
ENT0102TR Entamoeba histolytica Shontel DA
genomic DNA sequencing
BH130589.1 11135 bp cDNA
GSS.
Entamoeba histolytica
Entamoeba histolytica
Fukuyama: Entamoeba histolytica
(bases 1 to 907)
Determination of sequence and sequence
Unpublished (2001)
Contact: Professor J. L. J. J.
Department of Molecular Biology
The Institute for Genome Research
9712 Medical Center, Baltimore, MD 21205
Tel: 301 955 4200
Fax: 301 848 4544
Email: jlj@jimmy.duke.edu
Clones are derived from the Entamoeba histolytica library
DNA library
Seq primer: M1 reverse
Class: standard
High quality seq only, 8746.696
High quality seq only, 8746.696

FEATURES

Location/Qualifiers
1..907

Organism: "Batamada histolytica"
/strain="H910WS"

Notes: "H910WS" is a "H910WS" histolytic sheared DNA
clone from the "H910WS" histolytic sheared DNA
library. The "H910WS" histolytic sheared DNA
library was constructed at The
Institute for Genome Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
1967, and Diamond, B.S. (1993) Batamada histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
light size distribution (~2 kb). The V-11 method used for
the library construction is described in detail in Smith,
H.O., and Venner, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach by eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999)."

BASE COUNT

319 a 122 c 120 g 346 t

ORIGIN

Query Match

Post Local Similarity 100.0% Pred No. 27
Matches 27 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 129 AAAAAACATCTCTCCAAAT 150
|||||

130 768 AAAAAACATCTCTCCAAAT 737

RESULTS

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

ORIGIN

BASE COUNT

ORIGIN

Query Match

Post Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

129

AAAAACATCTCTCCAAAT

150

|||||

130

768

AAAAACATCTCTCCAAAT

737

RESULTS

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

ORIGIN

BASE COUNT

ORIGIN

Query Match

Post Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

129

AAAAACATCTCTCCAAAT

150

|||||

130

768

AAAAACATCTCTCCAAAT

737

RESULTS

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

ORIGIN

BASE COUNT

ORIGIN

Query Match

Post Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

129

AAAAACATCTCTCCAAAT

150

|||||

130

768

AAAAACATCTCTCCAAAT

737

RESULTS

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

ORIGIN

BASE COUNT

ORIGIN

Query Match

Post Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

129

AAAAACATCTCTCCAAAT

150

|||||

130

768

AAAAACATCTCTCCAAAT

737

RESULTS

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

ORIGIN

BASE COUNT

ORIGIN

Query Match

Post Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

129

AAAAACATCTCTCCAAAT

150

|||||

130

768

AAAAACATCTCTCCAAAT

737

RESULTS

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

ORIGIN

BASE COUNT

ORIGIN

Query Match

Post Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

129

AAAAACATCTCTCCAAAT

150

|||||

130

768

AAAAACATCTCTCCAAAT

737

RESULTS

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

ORIGIN

BASE COUNT

ORIGIN

Query Match

Post Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

129

AAAAACATCTCTCCAAAT

150

|||||

130

768

AAAAACATCTCTCCAAAT

737

RESULTS

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

ORIGIN

BASE COUNT

ORIGIN

Query Match

Post Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

129

AAAAACATCTCTCCAAAT

150

|||||

130

768

AAAAACATCTCTCCAAAT

737

RESULTS

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

ORIGIN

BASE COUNT

ORIGIN

Query Match

Post Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

129

AAAAACATCTCTCCAAAT

150

|||||

130

768

AAAAACATCTCTCCAAAT

737

RESULTS

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

ORIGIN

BASE COUNT

ORIGIN

Query Match

Post Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

129

AAAAACATCTCTCCAAAT

150

|||||

130

768

AAAAACATCTCTCCAAAT

737

RESULTS

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BASE COUNT

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Query Match

Post Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

QY

129

AAAAACATCTCTCCAAAT

150

|||||

130

768

AAAAACATCTCTCCAAAT

737

RESULTS

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

REFERENCE

1 (bases 1 to 538)

Author: Maria M. Hillier, Allen M., Bowles, M., Dietrich, N., Dubaque, T., Gotsal, S., Koyaba, P., Lacy, M., Le, M., Martin, J., Morris, M., Schellenger, K., Spector, M., Thel, T., Underwood, K., Moore, J., Thel, T., Wille, T., Lennon, G., Soares, R., Wilson, R., and Wierstra, K.

TITLE

The WashU-HMI Mouse EST Project

JOURNAL

Unpublished (1996)

Contact: Maria M/Mouse EST Project

COMMENT

WashU-HMI Mouse EST Project

Washington University, 660 S. Euclid, St. Louis, MO 63110

4444 Forest Park Parkway, Box 8001, St. Louis, MO 63110

Tel: 314 266 1406

Fax: 314 266 1810

Email: mouseest@wustl.wustl.edu

This clone is available royalty free through LIND: contact the

IMAGE Consortium (info@image.lind.gov) for further information.

MI1666840

Seq primer: -29ml 4 1002 BT from American

High quality sequence stop: 508.

Location/Qualifiers

1..548

Source: "Mus musculus"

Strain: "Taconic/63"

Ab_xref: "Taconic/63"

Ab_xref: "IMAGC/148048"

Ab_xref: "IMAGC/148048"

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Ab_xref: "IMAGC/148048"

Contact: Shuying Zhao

Department of Eukaryotic Genomics

155 Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: shuying@igrr.org

Clones are derived from the mouse BAC library KRC1-23. For BAC

library availability, please contact Peter de Jong

(peter@jimmy.med.utah.edu). Clones may be purchased from

IGRR for \$1000 per BAC. For more information, please contact

IGRR. This BAC is available for research purposes only. It is not

to be used for commercial purposes. The BAC is available for

research purposes only. It is not to be used for commercial

purposes. The BAC is available for research purposes only.

Seq primer: SP6

Class: BAC ends

Location/Qualifiers

1..557

Source: "Mus musculus"

Strain: "Taconic/63"

Ab_xref: "Taconic/63"

Ab_xref: "IMAGC/148048"

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Ab_xref: "IMAGC/148048"

Ab_xref: "IMAGC/148048"

GenCore version 5.1.3
Copyright (c) 1993 2002 CompuGen Ltd.

OM nuclele - nuclele search, using sw model

Run on: November 7, 2002, 08:51:15, Search time 1'30.36 Seconds

(without alignments)
10254 568 Million cell updates/sec

Title: US-09-755-633-6

Sequence: 1 ccaaatatattcattcgtt.....aatttcagtttttgccttg 610

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402879 residues

Total number of hits satisfying chosen parameters: 410x280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_bat:*
4: gb_bat:*
5: gb_bat:*
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40: gb_bat:*
41: gb_bat:*

score greater than or equal to the score of the
and is derived by analysis of the total score of

SUMMARIES

Result No.	Score	Query Match	Length (bp)	Hit
1	610	100.0	610	AF14919
2	485.8	66.5	485	AF14919
3	401.8	65.9	401	AX084948
4	379	62.1	379	AX084948
5	379	62.1	379	AX084948
6	379	62.1	379	AX084948
7	377.4	61.9	377	AX084948
8	364.4	59.7	364	AX084948
9	357.4	58.6	357	AX084948
10	341	55.9	341	AX084948
11	337.8	55.4	337	AX084948
12	329.8	54.1	329	AX084948
13	329.8	54.1	329	AX084948
14	326.6	53.5	326	AX084948
15	281.2	46.1	281	AX084948
16	280.2	45.9	280	AX084948
17	275.4	45.1	275	AX084948
18	273.8	44.9	273	AX084948
19	267.4	43.8	267	AX084948
20	250	41.0	250	AX084948
21	244.2	40.0	244	AX084948
22	242.4	39.9	242	AX084948
23	232	38.0	232	AX084948
24	232	38.0	232	AX084948
25	225.6	36.3	225	AX084948
26	221	36.2	221	AX084948
27	217.6	35.7	217	AX084948
28	217.6	35.7	217	AX084948
29	217.6	35.7	217	AX084948
30	217.6	35.7	217	AX084948
31	217.6	35.7	217	AX084948
32	217.6	35.7	217	AX084948
33	207.4	34.0	207	AX084948
34	207.4	34.0	207	AX084948
35	206.4	33.8	206	AX084948
36	206.4	33.8	206	AX084948
37	206.4	33.8	206	AX084948
38	186.4	29.3	186	AX084948
39	178.6	29.3	178	AX084948
40	172.2	28.2	172	AX084948
41	171.8	28.2	171	AX084948
42	168.6	27.3	168	AX084948
43	166.4	27.3	166	AX084948
44	166	27.2	166	AX084948
45	163.4	26.8	163	AX084948

ALIGNMENTS

RESULT 1
AF331919/c 610 bp mRNA
LOCUS AF331919
DEFINITION Canis familiaris Interleukin-5 mRNA, complete
ACCESSION AF331919
VERSION AF331919.1 GI11949180
KEYWORDS
SOURCE
ORGANISM Canis familiaris
Eukaryota; Metazoa; Mammalia; Canidae; Canis
Mammalia; Eukaryota; Metazoa; Mammalia; Canidae; Canis
Yang, S., Scollins, K.S., Webster, E., and Mural
Canine Interleukin-5: molecular character
expression of biologically active recombinant

JOURNAL
MEDLINE
21334408
PUBMED
11440634
REFERENCE
2 (bases 1 to 610)
AUTHORS
Yang, S.
TITLE
Direct Submission
SUBMITTED (25 DEC 2000) IMMEDIATELY
PROSPECT PARKWAY, FT COLLINS, CO 80525, USA
FEATURES
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1..610
5700R
1..610
29..433
/note="11-5"
/feature_start=1
/feature_end=433
/protein_id="F0410715.1"
/db_xref="GI:15919181"
/translation="MMDLNCGLAAGAAVAVAVINRRELVATGCTGTHREWL
IGENLMIPTEENRRLGCKREVEGLITLFRLEAVAKIPENLIPHLIFLA
KRGAEWRATKRLDYLQVRLVINTENIPES"
433..610
BASE COUNT
202 a 114 c 139 g 155 t
ORIGIN

Query Match 100.0% Score 610 DB 4 Length 610
Best Local Similarity 130 %; Pred. No. 1; Cons. 100%
Matches 610; Conserved 0; Mismatches 0; Indels 0; Gaps 0.

UY 1 CTCAAAATATTTATCTGTGGAAGTCAAAAGTAGAGATACATGAGAAATATTACTT 60
DB 610 CTCAAAATATTTATCTGTGGAAGTCAAAAGTAGAGATACATGAGAAATATTACTT 551
UY 61 GCGTCGTAAGCTTAGTAACTGCTGTAAGAAGTAACTGCTGCTGCTGCTGCTGCT 120
DB 550 GCGTCGTAAGCTTAGTAACTGCTGTAAGAAGTAACTGCTGCTGCTGCTGCTGCT 491
UY 121 CATGCCAAAGAGCATCTCTCTGTAAGATCTCCAGTACAAATAGAGATTTGTTGCA 180
DB 430 CATGCCAAAGAGCATCTCTCTGTAAGATCTCCAGTACAAATAGAGATTTGTTGCA 411
UY 181 AATCT 320
DB 410 AATCT 371
UY 241 GCTTGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 470 GCTTGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311
UY 401 TATTAAGCAAGTTTGGAAATAGTATAGCAAGCTCCGCTGCTGCTGCTGCTGCT 360
DB 410 TATTAAGCAAGTTTGGAAATAGTATAGCAAGCTCCGCTGCTGCTGCTGCTGCT 281
UY 391 CAAAGCTGATAGCTGTAAGAAAGCTGCTGTAAGCAAGCTGCTGCTGCTGCTGCT 420
DB 230 CAAAGCTGATAGCTGTAAGAAAGCTGCTGTAAGCAAGCTGCTGCTGCTGCTGCT 191
UY 421 AATAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 380
DB 130 AATAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 141
UY 481 TAAAGTCT 540
DB 130 TAAAGTCT 71
UY 541 AATGCCAATATATAGCAAGCTGTAAGCAAGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 70 AATGCCAATATATAGCAAGCTGTAAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCT 11
UY 601 GTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610
DB 10 GTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1

RESULT 2
AF025436 838 bp mRNA Human MAR 20 OCT 1998
1000S
CALIFICATION
ACCENSION
AF025436
VERSION
KEYWORDS
SOURCE
ORGANISM
Felis catus
Felis catus
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE
1 (bases 1 to 838)
Fauriol, E.A., Qiu, Y., Wells, T.N.C., Sander, P.J. and Camarero, J. Mercedo, B. Sequence and structural analysis of feline interleukin 5 cDNA
A. V. Res 1163 (1998) (1998)
MEDLINE
98452719
PUBMED
9781459
REFERENCE
2 (bases 1 to 838)
Fauriol, E.A., Qiu, Y., Wells, T.N.C., Sander, P.J. and Camarero, J. Mercedo, B. Submitted (15-SEP 1997) Medicine, University of Chicago, 5841 S. Maryland Avenue, Chicago, IL 60637, USA
location/Qualifiers
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/db_xref="taxon:9685"
/coll_type="Activated feline peripheral blood mononuclear cells"
1..838
/gene="11-5"
45..443
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/note="cytokine"
/feature_start=1
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/protein_id="AAC64505.1"
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/translation="KRMRLHGLAAGAAVAVAVINRRELVATGCTGTHREWL
IGENLMIPTEENRRLGCKREVEGLITLFRLEAVAKIPENLIPHLIFLA
KRGAEWRATKRLDYLQVRLVINTENIPES"
433..610
BASE COUNT
280 a 148 c 171 g 249 t
ORIGIN

Query Match 66.5% Score 405.8; DB 4 Length 838;
Best Local Similarity 86.8%; Pred. No. 6; Cons. 100%
Matches 498; Conserved 0; Mismatches 67; Indels 22; Gaps 4;
UY 81 AAGTCT 90
DB 588 AAGTCT 546
UY 91 AAGTCT 143
DB 545 AAGTCT 484
UY 144 CCAAGTCT 203
DB 144 CCAAGTCT 111
UY 481 AATAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 424
DB 481 AATAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 424
UY 204 TTAATAGCAAGCAAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAG 243
DB 424 TTAATAGCAAGCAAGTATAGTATAGTATAGTATAGTATAGTATAGTATAGTATAG 364
UY 264 CCGCAGCT 323
DB 463 CCGCAGCT 304
UY 824 GTTATCT 883
DB 403 GTTATCT 244

[illegible][illegible]

/db:ref "GI:2961561"
 /translation: "IGAAVSAIAVSPNBI VAPITALLSTPRLI IGVNLIPTP
 EHNHIGCTEEVNSCTPTI KNPVNSAVPKI PRNLIIEHIDSKKNI CKRREVE
 NFINIYDFELINI"
 BASE COUNT 114 a 74 c 71 g 95 t 1 others
 ORIGIN

Query Match 46.1% Score 281.2 DB 4 Length 354
 Host Local Similarity 87.5% Prod. No. 6,40-66
 Matches 307 Conservative 0 Mismatches 44 Indels 0 Gaps 0

```

97 200 GGTGTTAIIACCTAAATAAIACTTGCAGCTAGCTAGAACTTGGACCTGCATCTT 259
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
14 451 GGGTIIAAIAAAGTAAAGAAAAATTCAGGTAATTAGAAATTTTACTTGCATTT 292
97 260 TCTGCTTACACGCTTTTTTGGGCTTACGCTTTTATTAAGACGCACTTTGG 319
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
10 291 TTTCTCTAAAATTTTTTTTGGGCTTACGCTTTTATTAAGACGCACTTTGG 342
97 320 AATAGCTTATGCAAGCTCTGCTGGGCACTTGGTCTTCAATGGTCAATACCTGA 379
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
10 241 AAAATGTTTTTCATAGTACGCTGGGTAAGTATGCTTTAATGCTATACCTGA 172
97 380 AAAATTTCTTAATGTAACGTTGGATTTTATTTCAAGCTAGAAATCATCACTTC 439
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
10 171 AAGACCTCTCTCAATGCAATCTTCTTGATTTTATCTTCAAGCAATCAATCACTTC 112
97 440 CTATGCTTATGCAAGCTGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 499
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
10 111 CTGCTGCTTATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 52
97 500 CTATGCTTATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 550
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
10 51 CTATGCTTATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 1

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Search completed: November 7, 2002, 16:44:11
 Job time: 174.46 secs

GenCore version 5.1.3
Copyright (c) 1992 - 2002 CompuGen Ltd.

OM nucleotide - nucleotide search, using SW model

Run on: November 6, 2002, 10:41:56, Search time: 163.274 seconds

(without alignments)
8413,600 Million cell updates/sec

Title: US-09-755-633-6

Perfect score: 610

Sequence: 1 cctcaatattatcattcattgt.....aatcttagtttgcctctt 610

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapex: 1.0

Scanned: 2185233 seqs, 112599559 residues

Total number of hits satisfying chosen parameters: 4376478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

N:Geneseq_101002.*
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6: /S1082/gqj44r/gqj44r-seq/gqj44r-seq-emb1/NA_981.DAT.*
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Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	610	100.0	21	AA55546
2	610	100.0	21	AA55547
3	405.8	66.5	21	AA55548
4	402	65.9	21	AA55549
5	402	65.9	21	AA55550
6	401.8	65.9	21	AA55551
7	379	62.1	21	AA55552
8	379	62.1	21	AA55553
9	379	62.1	21	AA55554

10	379	62.1	21	AA55555
11	379	62.1	21	AA55556
12	364.4	59.7	21	AA55557
13	345	56.6	21	AA55558
14	345	56.6	21	AA55559
15	314.2	51.5	21	AA55560
16	293.8	48.2	21	AA55561
17	275.7	45.3	21	AA55562
18	252	41.3	21	AA55563
19	249.4	40.9	21	AA55564
20	232	38.0	21	AA55565
21	217.6	35.7	21	AA55566
22	217.6	35.7	21	AA55567
23	217.6	35.7	21	AA55568
24	217.6	35.7	21	AA55569
25	209.6	34.0	21	AA55570
26	207.4	34.0	21	AA55571
27	206.4	33.8	21	AA55572
28	206.4	33.8	21	AA55573
29	196.4	32.2	21	AA55574
30	194.6	31.9	21	AA55575
31	194.2	31.8	21	AA55576
32	181.4	29.7	21	AA55577
33	178.6	29.3	21	AA55578
34	172.2	28.2	21	AA55579
35	168.6	27.6	21	AA55580
36	166.4	27.3	21	AA55581
37	166	27.2	21	AA55582
38	163.4	26.8	21	AA55583
39	162.2	26.6	21	AA55584
40	161.6	26.5	21	AA55585
41	161.6	26.5	21	AA55586
42	161.6	26.5	21	AA55587
43	153	25.1	21	AA55588
44	152.4	25.0	21	AA55589
45	152.4	25.0	21	AA55590

REFERENCES

AA55546	1: MAE 2000 (first entry)
AA55547	1: MAE 2000 (first entry)
AA55548	1: MAE 2000 (first entry)
AA55549	1: MAE 2000 (first entry)
AA55550	1: MAE 2000 (first entry)
AA55551	1: MAE 2000 (first entry)
AA55552	1: MAE 2000 (first entry)
AA55553	1: MAE 2000 (first entry)
AA55554	1: MAE 2000 (first entry)
AA55555	1: MAE 2000 (first entry)
AA55556	1: MAE 2000 (first entry)
AA55557	1: MAE 2000 (first entry)
AA55558	1: MAE 2000 (first entry)
AA55559	1: MAE 2000 (first entry)
AA55560	1: MAE 2000 (first entry)
AA55561	1: MAE 2000 (first entry)
AA55562	1: MAE 2000 (first entry)
AA55563	1: MAE 2000 (first entry)
AA55564	1: MAE 2000 (first entry)
AA55565	1: MAE 2000 (first entry)
AA55566	1: MAE 2000 (first entry)
AA55567	1: MAE 2000 (first entry)
AA55568	1: MAE 2000 (first entry)
AA55569	1: MAE 2000 (first entry)
AA55570	1: MAE 2000 (first entry)
AA55571	1: MAE 2000 (first entry)
AA55572	1: MAE 2000 (first entry)
AA55573	1: MAE 2000 (first entry)
AA55574	1: MAE 2000 (first entry)
AA55575	1: MAE 2000 (first entry)
AA55576	1: MAE 2000 (first entry)
AA55577	1: MAE 2000 (first entry)
AA55578	1: MAE 2000 (first entry)
AA55579	1: MAE 2000 (first entry)
AA55580	1: MAE 2000 (first entry)
AA55581	1: MAE 2000 (first entry)
AA55582	1: MAE 2000 (first entry)
AA55583	1: MAE 2000 (first entry)
AA55584	1: MAE 2000 (first entry)
AA55585	1: MAE 2000 (first entry)
AA55586	1: MAE 2000 (first entry)
AA55587	1: MAE 2000 (first entry)
AA55588	1: MAE 2000 (first entry)
AA55589	1: MAE 2000 (first entry)
AA55590	1: MAE 2000 (first entry)

0Y 443 GCTATGACCAAGTTCAGTACGAGCAGCTTCAAGCTCTCTGACCAAGCTAT 504
 1 111111 11111111 111111 111111 111111 111111 111111
 0B 182 GCTATGACCAAGTTCAGTACGAGCAGCTCTCTGACCAAGCTAT 123
 1 111111 11111111 111111 111111 111111 111111 111111
 0Y 505 GATGGATTTCTACAGCAAGGAGAGAAATAGCAGCCCAAGAGTACCAACTCA 504
 1 111111 111111 111111 111111 111111 111111 111111
 0B 122 GCTGGATTTCTGAGGATGAGAGAGAAATAGCAGCCCAAGAGTACCAACTCA 63
 1 111111 111111 111111 111111 111111 111111 111111
 0Y 505 ATTGAAGGATTCAGTACGAGCAGCTTCAAGCTCTCTGACCAAGCTAT 609
 1 111111 111111 111111 111111 111111 111111 111111
 0B 62 ATTGAAGGATTCAGTACGAGCAGCTTCAAGCTCTCTGACCAAGCTAT 18
 1 111111 111111 111111 111111 111111 111111 111111

RESULT 2

US-08-629-643A-4/c
 Sequence 4, Application US/08629643A
 Patent No. 6025649

GENERAL INFORMATION:
 APPLICANT: Lee, J. L.
 APPLICANT: Lee, N. A.
 TITLE OF INVENTION: IL-5 TRANSDUCTION MOUSE
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESS: Schwabman, Leonard, Westport 5 Kitch, P. A.
 STREET: P. O. Box 2938
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 55402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US08629643A
 FILING DATE:
 CLASSIFICATION: B00
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/279,111
 FILING DATE: 09-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Viksnious, Ann S
 REGISTRATION NUMBER: 37,748
 REFERENCE/KEY NUMBER: 150,1676-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-359-3260
 TELEFAX: 612-359-3263
 TELEX:
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1534 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURES:
 NAME/KEY: mol_1peptide
 LOCATION: 104...442
 OTHER INFORMATION:
 US-08-629-643A-4

Query Match: 35.74; Score 217.6; DR 3; Length 1534.
 Best local similarity: 59.24; Pctd. No. 170-583

Match: 412; Conservative 9; Mismatches 136; Indels 3; Gaps 1.

0Y 159 AATAAATGCTTGGTCAATTCGGGTCGACATGCGTCTTATATACCAAGCA 218
 1 111111 111111 111111 111111 111111 111111 111111
 0B 444 AATAAATGCTTGGTCAATTCGGGTCGACATGCGTCTTATATACCAAGCA 405
 1 111111 111111 111111 111111 111111 111111 111111
 0Y 219 AATAAATGCTTGGTCAATTCGGGTCGACATGCGTCTTATATACCAAGCA 278
 1 111111 111111 111111 111111 111111 111111 111111

0B 404 ACTCTTGACGATATCCAGAACTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 345
 1 111111 111111 111111 111111 111111 111111 111111
 0Y 279 TTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 348
 1 111111 111111 111111 111111 111111 111111 111111
 0B 444 TTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 285
 1 111111 111111 111111 111111 111111 111111 111111
 0Y 439 GCGCTGCGGCAATTTGGGTTTTCATATGCTGCTGCTGCTGCTGCTGCTGCT 498
 1 111111 111111 111111 111111 111111 111111 111111
 0B 284 GCGCTGCGGCAATTTGGGTTTTCATATGCTGCTGCTGCTGCTGCTGCTGCT 225
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 0Y 439 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 458
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 0B 224 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 165
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 0Y 519 GAGCAAAAGGCAAAACAATAGCAGCCCAAGAGTACCAACTCAAGAGCTTC 578
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 0B 104 TGCGAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 48
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 0Y 579 TCATAGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 609
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 0B 47 TCATAGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 17
 1 111111 111111 111111 111111 111111 111111 111111

RESULT 3

US-09-155-884-4/c
 Sequence 4, Application US/09155884
 Patent No. 6215040

GENERAL INFORMATION:
 APPLICANT: James J. Lee et al.
 TITLE OF INVENTION: IL-5 TRANSDUCTION MOUSE
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESS: Schwabman, Leonard, Westport 5 Kitch, P. A.
 STREET: P. O. Box 2938
 CITY: Minneapolis
 STATE: MN
 COUNTRY: USA
 ZIP: 55402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/079,155-884
 FILING DATE: unknown
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/079,205,922
 FILING DATE: 09-APR-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Viksnious, Ann S
 REGISTRATION NUMBER: 37,748
 REFERENCE/KEY NUMBER: 150,1676-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 612-359-3260
 TELEFAX: 612-359-3061
 TELEX:
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1534 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURES:
 NAME/KEY: mol_1peptide
 LOCATION: 104...442
 OTHER INFORMATION:



Clonal Distribution: Researchers may obtain clones from Research Genetics (www.research.com).

Seq primer: M13 FORWARD
pMTA Vrs.

FEATURES
SOURCE location/GenBank
1..504

/organism "Mus musculus"
/strain "C57BL/6J"
/db_xref "taxon:10090"
/clone "M13-P4-dbc-08-1-0M"

Site host: "phlox (the phospholipase)"
Note: "Vector: pMT4-Pac (PharMacia) with a modified linker. Site: Not in site 2. Host: The M13 P4 library is derived from embryo at gestational day 14. For a detailed description of the library from which this clone was derived, please visit our web site at <http://www.research.com>"

FASTA: M13-P4
FASTA: M13-P4-postclonation-14_conceptus
TAG_Seq-ACCTAC

BASE COUNT 147 a 95 c 69 g 192 t

Query Match 27.0% Score 164.8; DB 14; Length 503;

Best local similarity 77.3% Prod. No. 3,904,4;
Matches 215; Unsuccessful 0; Mismatches 57; Indels 6; Gaps 1;

QY 11 TTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 70

DB 226 TTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 285

QY 71 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 180

DB 286 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 145

QY 141 AAATATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 184

DB 446 AAATATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 405

QY 185 TCGATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 244

DB 409 TCGATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 465

QY 245 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 282

DB 466 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 503

QY 111 TTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 180

DB 226 TTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 285

QY 71 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 180

DB 286 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 145

QY 141 AAATATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 184

DB 446 AAATATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 405

QY 185 TCGATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 244

DB 409 TCGATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 465

QY 245 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 282

DB 466 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 503

QY 111 TTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 180

DB 226 TTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 285

QY 71 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 180

DB 286 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 145

QY 141 AAATATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 184

DB 446 AAATATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 405

d'Etude du Polymorphisme Humain) with funding provided by a Merit project grant. The HMA was prepared from embryos by Alain Bouchon and Genevieve Payan. It has been constructed in the vector pMT4-Pac.

FEATURES
SOURCE location/GenBank
1..1101

/organism "Mus musculus"
/strain "C57BL/6J"
/db_xref "taxon:10090"
/clone "M13-P4-dbc-08-1-0M"

Site host: "phlox (the phospholipase)"
Note: "Vector: pMT4-Pac (PharMacia) with a modified linker. Site: Not in site 2. Host: The M13 P4 library is derived from embryo at gestational day 14. For a detailed description of the library from which this clone was derived, please visit our web site at <http://www.research.com>"

FASTA: M13-P4
FASTA: M13-P4-postclonation-14_conceptus
TAG_Seq-ACCTAC

BASE COUNT 247 a 84 c 159 g 263 t 448 others

Query Match 7.2% Score 43.8; DB 17; Length 1101;

Best local similarity 22.4% Prod. No. 0,71;
Matches 215; Unsuccessful 0; Mismatches 57; Indels 6; Gaps 1;

QY 11 TTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 70

DB 226 TTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 285

QY 71 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 180

DB 286 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 145

QY 141 AAATATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 184

DB 446 AAATATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 405

QY 185 TCGATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 244

DB 409 TCGATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 465

QY 245 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 282

DB 466 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 503

QY 111 TTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 180

DB 226 TTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 285

QY 71 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 180

DB 286 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 145

QY 141 AAATATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 184

DB 446 AAATATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 405

QY 185 TCGATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 244

DB 409 TCGATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 465

QY 245 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 282

DB 466 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 503

QY 111 TTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 180

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QY 71 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 180

DB 286 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 145

QY 141 AAATATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 184

DB 446 AAATATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 405

QY 185 TCGATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 244

DB 409 TCGATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 465

QY 245 GCTTATGCTGCTGAGTATTAAGTATTAATGCTGAAATTTATGCTGCTGAA 282

genomic DNA isolated from fresh cultures of *B. histolytica* using a method described by Clark and Hammond (Clark, C.C. and Diamond, L.S. (1994) *Entamoeba histolytica*: a method for isolate identification. *Exp. Parasitol.* 77:350-353). The DNA was mechanically sheared to give a

fragment size distribution (2 kb). The λ phage method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In *Genome Sequencing: A Practical Approach*, eds. M. Vaudin and R. Barrell, Oxford University Press, 1999).

BASE COUNT 185 a 64 c 194 g 184 t

Query Match 6.6% Score 40.4; Db 17; Length 926;

Best local similarity 48.6%; Prev. No. 5.4; Mismatches 146; Indels 1; Gaps 1.

Matches 139; Conservative 0; Mismatches 146; Indels 1; Gaps 1.

43 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 102

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 746

47 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 162

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 676

49 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 221

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 616

47 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 281

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 556

49 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 342

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 510

47 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 381

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 510

49 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 442

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 510

47 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 503

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 510

49 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 564

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 510

47 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 625

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 510

49 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 686

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 510

47 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 747

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 510

49 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 808

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 510

47 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 869

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 510

49 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 930

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 510

47 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 991

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 510

49 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 1052

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 510

/zone lib "wong rice bac library"
/issue type "leaf"
/lab host "E. coli DH10B"

/note "Vector: pBluescript SK(-); HindIII; Site 2; HindIII. Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arunachalam and Kato, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genome studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 16,864 clones with an average insert size of 128.5 kb providing 19.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 15,432 clones (doubly spotted), represent the whole library for colony screening."

BASE COUNT 184 a 107 c 130 g 202 t

Query Match 6.6% Score 40.2; Db 17; Length 623;

Best local similarity 48.1%; Prev. No. 5.4; Mismatches 123; Indels 0; Gaps 0;

Matches 114; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

49 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 410

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 471

47 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 471

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 471

49 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 532

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 471

47 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 593

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 471

49 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 654

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 471

47 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 715

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 471

49 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 776

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 471

47 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 837

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 471

49 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 898

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 471

47 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 959

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 471

49 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 1020

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47 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 1081

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 471

49 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 1142

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 471

47 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 1203

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 471

49 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 1264

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 471

47 TGGTGAATAATTACTTGTCTGCTGAAGTTACTTAACTGGCAATTAATCCCTACTG 1325

DB TCGTAAATAATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 471



GenCore version 5.1.3
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GM nucleic - nucleic search, using sw model

Run on: November 7, 2002 08:51:15 : Search time 1:40:27 Seconds

(without alignments)
10260.168 Million cell updates/sec

Title: US-09-755-633-7

Perfect Score: 402
Sequence: 1 aagagagatggttctggaatttcccccccccaggatggagacagcagatgaagtl 402

Scoring table:

Gapop 60 0 : Gapext 60 0

Sequences: 2054640 seqs, 14551402678 residues

Word size: 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 9

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database:

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Gremlin:
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2: qb_bla*
3: qb_bla*
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41: qb_bla*

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pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the
and is derived by dividing the total score of

SUMMARIES

Result No.	Score	Query Match	Query Length	Hit	Score	Query Match	Query Length	Hit
1	402	100.0	402	1	402	100.0	402	1
2	393	97.8	402	2	393	97.8	402	2
3	271	67.4	402	3	271	67.4	402	3
4	250	62.2	402	4	250	62.2	402	4
5	144	35.8	402	5	144	35.8	402	5
6	43	10.7	402	6	43	10.7	402	6
7	43	10.7	402	7	43	10.7	402	7
8	42	10.4	402	8	42	10.4	402	8
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11	41	10.2	402	11	41	10.2	402	11
12	41	10.2	402	12	41	10.2	402	12
13	40	10.0	402	13	40	10.0	402	13
14	30	7.5	402	14	30	7.5	402	14
15	28	7.0	402	15	28	7.0	402	15
16	26	6.5	402	16	26	6.5	402	16
17	22	5.5	402	17	22	5.5	402	17
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22	22	5.5	402	22	22	5.5	402	22
23	22	5.5	402	23	22	5.5	402	23
24	22	5.5	402	24	22	5.5	402	24
25	22	5.5	402	25	22	5.5	402	25
26	22	5.5	402	26	22	5.5	402	26
27	22	5.5	402	27	22	5.5	402	27
28	22	5.5	402	28	22	5.5	402	28
29	22	5.5	402	29	22	5.5	402	29
30	22	5.5	402	30	22	5.5	402	30
31	22	5.5	402	31	22	5.5	402	31
32	22	5.5	402	32	22	5.5	402	32
33	22	5.5	402	33	22	5.5	402	33
34	22	5.5	402	34	22	5.5	402	34
35	22	5.5	402	35	22	5.5	402	35
36	22	5.5	402	36	22	5.5	402	36
37	22	5.5	402	37	22	5.5	402	37
38	22	5.5	402	38	22	5.5	402	38
39	22	5.5	402	39	22	5.5	402	39
40	21	5.2	402	40	21	5.2	402	40
41	21	5.2	402	41	21	5.2	402	41
42	21	5.2	402	42	21	5.2	402	42
43	21	5.2	402	43	21	5.2	402	43
44	21	5.2	402	44	21	5.2	402	44
45	21	5.2	402	45	21	5.2	402	45

ALIGNMENTS

RESULT 1
AF331919
LOCUS
DEFINITION
ACCESSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

AF331919 616 bp mRNA
Canis familiaris Interleukin 5 mRNA, complete cds
AF331919.1 616 bp mRNA
Canis familiaris
Canis familiaris
Baskarjula, Mohanraj, Theodor, Granat, V
Mammalia: Canidae: Canis: Canis familiaris
I (Baskarjula, Mohanraj, Theodor, Granat, V)
Yang, S., Saito, K., Weber, F., and P. S.
Canine Interleukin 5: molecular characterization
expression of functionally active recombinant

[illegible][illegible]

COGENT	06011647 A 1 15 FEB 2001
ORIGIN	IPFAX LABORATORIES, INC. (US)
FEATURES	CS 000 24 2001 THIS MESSAGE WAS NOT RECORDED AT 14185501.
SOURCE	1. 405 Locality/Qualifiers
	/organism "Gambusia holbrooki"
	"Ch_xref "Eucyon9615"
DATE/TIME	141 a 77 c 94 q 103 t
ORIGIN	
Query Match	97.8%
Query Match Similarity	100.0%
Matches	393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

U7	1	ATGAAATAGCTTCGAATTGGATTTGTACGCTTACAGGTACTAATAGTTCTCGCTTT	60
U8	1	ATGAAATAGCTTCGAAATTTGATCTTTTAGCTCTTAGGCTACTAATAGTTCTCGCTTT	60
U9	1	GCTCAATAAATCAGCATCAATATATGCAAGAAAGATCCCAATCTCTCTACTGAT	120
U4	1	TTTCTAATAAATATATGAAATATATATGCAAGAAAGATCCCAATCTCTCTACTGAT	120
U7	121	CGAACTTGAGCTGATAGGCCATGGAAGCTGATGATTTCTACTCTGAAAATAAAAATCAC	180
U8	121	CGAACTTGAGCTGATAGGCCATGGAAGCTGATGATTTCTACTCTGAAAATAAAAATCAC	180
U9	181	CACATGTCGATTAAGAAGATTTTTCAGGCTATATGCATATTCGAAATAGCGAAATGGCGCA	240
U4	181	CACATGTCGATTAAGAAGATTTTTCAGGCTATATGCATATTCGAAATAGCGAAATGGCGCA	240
U7	241	GCGGAGCATCTCCATAAATCATATGCTAAAGATCTCTTAAATAAAGAACATATAGAGCGT	300
U8	241	GCGGAGCATCTCCATAAATCATATGCTAAAGATCTCTTAAATAAAGAACATATAGAGCGT	300
U9	301	CAAAAAAAGCTGTGCAGAGAAAGAAATGCGAGATGCGAAAGCTGTACATCTACGCAA	360
U4	301	CAAAAAAAGCTGTGCAGAGAAAGAAATGCGAGATGCGAAAGCTGTACATCTACGCAA	360
U7	361	GTATTCTTGCTGTAAATAACAATCAATGGAGCA	420
U8	361	GTATTCTTGCTGTAAATAACAATCAATGGAGCA	420
RESULT 4			
AF091133		456 bp mRNA linear MAM 04-AUG-1998	
DEFINITION		Canis familiaris interleukin-5 mRNA, partial cds.	
LOCUS		AF091133	
FEATURES			
ACCSSION		AF091133	
VERSION		AF091133.1 GI:5690204	
KEYWORDS			
SOURCE			
ORGANISM		Canis familiaris.	
		Canis familiaris	
		Eukaryota; Mammalia; Carnivora; Euteleostomi;	
		Mammalia; Eutheria; Carnivora; Fissipedes; Canidae; Canis.	
REFERENCE		1 (bases 1 to 356)	
AUTHORS		Berman A.J., Helms G.E., Harley R., Hall B.L. and Day M.J.	
TITLE		Cloning and sequencing of canine interleukin-5	
JOURNAL		Unpublished	
BOOKID		2 (bases 1 to 356)	
REMARKS		German A.J., Helms G.E., Harley R., Hall B.L. and Day M.J.	
AUTHOR		Direct Submission	
DATE		Submitted (12-SEP-1998) Department of Clinical Veterinary Science,	
UNIVERSITY		University of Bristol, Langford House, Langford, Bristol, North	
PROJECT		Somerset BS40 5DU, United Kingdom	
FEATURES			
SOURCE		Exonology/familiars	
		1..356	
		/organism="Canis familiaris"	
		/db_xref="taxon:9615"	
		ct..>356	
		/note="11-5"	
		/product "interleukin-5"	
		/protein_id="AA010991.1"	


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KEYWORDS
SOURCE
ORGANISM
Ovis aries.
Eukaryote; Metazoa; Chordata; Canidae; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Puminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE
1 (bases 1 to 520)
AUTHORS
Szymanski, David M., J., McManus, P. G., Hutzel, and Wood, P. R.
TITLE
Cloning of ovine interleukin-5 cDNA
JOURNAL
Immunology (1995)
2 (bases 1 to 520)
AUTHORS
Szymanski, David M., J.
TITLE
Direct Submission
JOURNAL
Submitted (08-AUG-1995) Hong-Pong Snow, Animal Health, CSIRO,
Corner of Flemington Rd and Park Drive, Melbourne, Vic 3052,
Australia
FEATURES
SOURCE
1..520
/organism="Ovis aries"
/zb_xref="taxon:9940"
46..444
CDS
1..520
/feature_start=1
/product="interleukin-5"
/protein_id="AAC99991.1"
/zb_xref="GI:4096664"
41..520
Direct Submission
JOURNAL
Submitted (08-AUG-1995) Hong-Pong Snow, Animal Health, CSIRO,
Corner of Flemington Rd and Park Drive, Melbourne, Vic 3052,
Australia
BASE COUNT
156 a 99 c 134 g 141 t
ORIGIN
Query Match
10.7% Score 43; BB 4; Length 520;
Best Local Similarity 100.0%; Prod. No. 1-10-12;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

U7 74 CCAATATATACAGTGGTGCATACAGCTTACACATCTCTCTCCAC 115
|||||
U6 113 CCAATATATACAGTGGTGCATACAGCTTACACATCTCTCTCCAC 115

RESULT 7
LOCUS
OALV1 1140 bp DNA linear MAR 23 AUG-2002
DEFINITION
Ovis aries interleukin-5 (115) gene, exons 1 and 2.
ACCESSION
U7052.1 GI:897558
VERSION
017052.1
KEYWORDS
1 of 2
SEGMENT
1
SOURCE
Sheep
ORGANISM
Ovis aries
Eukaryote; Metazoa; Chordata; Canidae; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Puminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE
1 (bases 1 to 1140)
AUTHORS
Bryson, C. E., Viney, E., Brandon, M., and Boyd, A. W.
TITLE
Structure of the sheep interleukin-5 gene.
JOURNAL
Immunology (1995)
2 (bases 1 to 1140)
AUTHORS
Bryson, C. E.
TITLE
Direct Submission
JOURNAL
Submitted (08-NOV-1994) Claire E. Bryson, Department of Veterinary
Science, University of Melbourne, Parkville, Vic 3010, Australia.
FEATURES
SOURCE
1..1140
/organism="Ovis aries"
/zb_xref="taxon:9940"
439..347
DATA_signal
/region="115"
489..395
/region="115"
-170..607
-170..607
/region="115"

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Oxoni
/number=1
824..856
/region="115"
/number=2
BASE COUNT
463 a 168 c 198 g 411 t
ORIGIN
Query Match
10.7% Score 43; BB 4; Length 1140;
Best Local Similarity 100.0%; Prod. No. 1-10-12;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

U7 74 CCAATATATACAGTGGTGCATACAGCTTACACATCTCTCTCCAC 115
|||||
U6 547 CCAATATATACAGTGGTGCATACAGCTTACACATCTCTCTCCAC 579

RESULT 8
LOCUS
SSC010088 1071 bp mRNA linear MAR 03 FEB 2000
DEFINITION
Sus scrofa mRNA for Interleukin-5.
ACCESSION
A010088
VERSION
A010088.2 GI:6911700
KEYWORDS
IL-5 gene; interleukin-5.
SOURCE
Sus scrofa.
ORGANISM
Sus scrofa
Eukaryote; Metazoa; Chordata; Canidae; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Artiodactyla; Suidae; Suidae; Sus.
REFERENCE
1 (bases 1 to 405)
AUTHORS
Sylvén, H., Malmgren, M., and van der
ploeg, J.
TITLE
Molecular cloning, expression, and purification of pig
interleukin-5
JOURNAL
Immunogenetics 51 (1): 59-64 (2000)
MEDLINE
20130134
PIRME
10663563
REFERENCE
2 (bases 1 to 405)
AUTHORS
Sylvén, H.
TITLE
Direct Submission
JOURNAL
Submitted (11-AUG-1998) Sylvén H., Department of Laboratory
Medicine, Division of Clinical Immunology, Karolinska
Institute, Karolinska Hospital, S-141 76 Stockholm, SWEDEN
Revised by author
3 (bases 1 to 405)
REFERENCE
Sylvén, H.
TITLE
Direct Submission
JOURNAL
Submitted 193-FEB-2000) Sylvén H., Department of Laboratory
Medicine, Division of Clinical Immunology, Karolinska
Institute, Karolinska Hospital, S-141 76 Stockholm, SWEDEN
In Feb 77, 2000 this sequence version replaced GI:2782796.
FEATURES
SOURCE
1..405
/organism="Sus scrofa"
/zb_xref="taxon:9933"
1..405
CDS
1..405
/region="115"
1..405
/region="115"
/feature_start=1
/product="interleukin-5"
/protein_id="CAI20611.2"
/zb_xref="GI:6911701"
73..405
Direct Submission
JOURNAL
Submitted (08-NOV-1994) Sylvén H., Department of Laboratory
Medicine, Division of Clinical Immunology, Karolinska
Institute, Karolinska Hospital, S-141 76 Stockholm, SWEDEN
In Feb 77, 2000 this sequence version replaced GI:2782796.
BASE COUNT
133 a 72 c 93 g 107 t
ORIGIN
Query Match
10.4% Score 42; BB 4; Length 405;
Best Local Similarity 100.0%; Prod. No. 1-9-12;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

U7 74 CCAATATATACAGTGGTGCATACAGCTTACACATCTCTCTCCAC 115
|||||

```

DB 74 GCATGATATAGCTGCTGAGACAGACTTGCACACTGCTGCA 115

RESULT 9
SSC134452 529 bp mRNA linear MAR 09-FEB 2000

DEFINITION
Sus scrofa mRNA for interleukin 5.
ACCESSION
AL334452
VERSION
AL334452.2 G15667055
KEYWORDS
IL-5 gene; interleukin 5.
SOURCE
Sus scrofa.
ORGANISM
Sus scrofa.
Eukaryota; Metazoa; Chordata; Graziata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae Sus.

REFERENCE
AUTHORS
1 (bases 1 to 529)
Henderson, P. K. (2000) Henderson, J., Johansen, E., Jorgensen, S. and

TITLE
Sus scrofa mRNA for interleukin 5

JOURNAL
Unpublished

REFERENCE
AUTHORS
2 (bases 1 to 529)
Johansen, E. K.

TITLE
Direct Submission

JOURNAL
Submitted (02-MAR-1999) Johansen, E. K., Department of Biochemistry
and Immunology, Danish Veterinary Laboratory, Copenhagen 27, DK-1793
Copenhagen V, DENMARK

REMARK
3 (bases 1 to 529)
revised by 131

REFERENCE
AUTHORS
Johansen, E. K.

TITLE
Direct Submission

JOURNAL
Submitted (07-FEB-2000) Johansen, E. K., Department of Biochemistry
and Immunology, Danish Veterinary Laboratory, Rulowvej 27, DK-1790
Copenhagen V, DENMARK

COMMENT
On Feb 11, 2000 this sequence version replaced 313452325.
FEATURES
source
1..529
location/qualifiers

/organism="Sus scrofa"

/db_xref="taxon:9823"

/cell_type="lymph node"

/issue_type="unq"

1..405

/gene="IL-5"

1..405

/gene="IL-5"

/cds="start"

/protein_id="CAE38328.1"

/db_xref="GI:4469327"

/transcript="NM011818.1"

108NM181818.1 (FEB 2000) NCBI

108NM181818.1 (FEB 2000) NCBI

108NM181818.1 (FEB 2000) NCBI

108NM181818.1 (FEB 2000) NCBI

108NM181818.1 (FEB 2000) NCBI

108NM181818.1 (FEB 2000) NCBI

108NM181818.1 (FEB 2000) NCBI

108NM181818.1 (FEB 2000) NCBI

108NM181818.1 (FEB 2000) NCBI

108NM181818.1 (FEB 2000) NCBI

108NM181818.1 (FEB 2000) NCBI

REFERENCE
AUTHORS
1 (bases 1 to 405)
Vandegriff, E., Hodges, K. J., and O'Keefe, J. K.

TITLE
Direct Submission

JOURNAL
Submitted (27-MAY-1998) VMP, LSU School of
South Stadium Drive, Baton Rouge, LA 70803

REFERENCE
AUTHORS
2 (bases 1 to 405)
Vandegriff, E., Hodges, K. J., and O'Keefe, J. K.

TITLE
Direct Submission

JOURNAL
Submitted (27-MAY-1998) VMP, LSU School of
South Stadium Drive, Baton Rouge, LA 70803

REMARK
Sequence update to submitter
on Jul 28, 1998 this sequence version (VPI
1..405
location/qualifiers

/organism="Sus scrofa"

/db_xref="taxon:9823"

1..405

/gene="IL-5"

1..405

/cds="start"

/protein_id="AA27616.1"

/db_xref="GI:4469327"

/transcript="NM011818.1"

108NM181818.1 (FEB 2000) NCBI

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108NM181818.1 (FEB 2000) NCBI

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108NM181818.1 (FEB 2000) NCBI

108NM181818.1 (FEB 2000) NCBI

108NM181818.1 (FEB 2000) NCBI

108NM181818.1 (FEB 2000) NCBI

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108NM181818.1 (FEB 2000) NCBI

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108NM181818.1 (FEB 2000) NCBI

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108NM181818.1 (FEB 2000) NCBI

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108NM181818.1 (FEB 2000) NCBI

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108NM181818.1 (FEB 2000) NCBI

108NM181818.1 (FEB 2000) NCBI

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108NM181818.1 (FEB 2000) NCBI



RESULT 3

AAZ55546

ID AAZ55546 standard: cDNA: 610 BP.

XX AAZ55546:

XX 14-MAR-2000 (first entry)

XX Canine interleukin-5 (IL-5) cDNA.

XX Interleukin-5, IL-5; antibody: canine; inhibitor; immune response;

XX immunoregulation; tumour; cancer; autoimmune disease; allergic; ss.

XX Canis familiaris

XX Key: Local only/Global only

XX CDS 29,443

XX /Feature=3

XX /product= "Canine IL-5"

XX W09961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999: 99W0-0811942

XX 29-MAY-1998: 98US-0087306.

XX (HESK-) HESKA CORP.

XX Sim G., Yang S., Drexler M.J., Wonderling RS;

XX MPI: 2690-072623706

XX P-PSDB: AAV58219.

XX

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RESULT 4

AAZ55547/C

ID AAZ55547 standard: cDNA: 610 BP.

XX AAZ55547:

XX 14-MAR-2000 (first entry)

XX Canine interleukin-5 (IL-5) cDNA complement.

XX Interleukin 5, IL-5; antibody: canine; inhibitor;

XX immunoregulation; tumour; cancer; autoimmune disease

XX Canis familiaris.

XX Key: Local only/Global only

XX CDS 29,443

XX /Feature=3

XX /product= "Canine IL-5"

XX W09961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999: 99W0-0811942

XX 29-MAY-1998: 98US-0087306.

XX (HESK-) HESKA CORP.

XX Sim G., Yang S., Drexler M.J., Wonderling RS;

XX MPI: 2690-072623706

XX P-PSDB: AAV58219.

XX

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XX

XX

XX

XX

XX

Query Match

100.00

Seqs: 402

DB: 21

Local: 610

Best Local Similarity: 100.00

Prct No: 6

Seqs: 402

Matches: 402

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

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AA424265
ID AA424265 standard; DNA; 838 BP.
XX
XX
AC AA424265;
XX
XX
DT 31-MAR-2000 (first entry)
XX
XX
DE Porcine IL-5 DNA.
XX
XX
KW P13: VACCINE; cysticercosis; protective antigen; ccl; cc2; cc4;
KW TETRAI (cysticercosis); gamma interferon; IFN-gamma; interleukin 5;
KW IL-5; ss.
XX
XX
OS SUS SCROTA.
XX
XX
FN CN1231339-A.
XX
XX
PD 13-OCT-1999.
XX
XX
PE 29-JAN-1999; 99CN-0113447
XX
XX
PR 29-JAN-1999; 99CN-0113447.
XX
XX
FA (OYIW-) UNIV NO 2 MILITARY MEDICAL PLA.
XX
XX
FI Sun S. Bai J.
XX
XX
DR WPI: 2000-097904/08
XX
XX
PT Nucleic acid vaccine for cysticercosis co-constructed by human and pig
XX
XX
PS Claim 3; Page 9; 21pp; Chinese.
XX
XX
CC This invention describes a novel nucleic acid vaccine for preventing and
CC curing human and pig cysticercosis. The invention involves the
CC formation of a eukaryotic expression plasmid from fusion transcript
CC expression unit consisting of three protective antigen genes (ccl, cc2
CC and cc4) of pig tetra cysticercosis and coexpression unit of related cell
CC factor gamma interferon (IFN-gamma) and pig interleukin 5 (IL-5) genes.
CC The production and purification process of said nucleic acid vaccine is
CC simple and convenient, the physical and chemical properties of the
CC vaccine are stable, and the vaccine is easy to store and transport, and
CC possesses effective immunological protective function for human and pig
CC cysticercosis. This sequence represents the pig IL-5 gene used in the
CC method of the invention.
XX
XX
SQ Sequence 838 BP; 280 A; 148 C; 171 G; 239 T; 0 other.

Query Match: 100.0%, Score 11, Len 27, Length 838,
Best local Similarity: 100.0%; Pred. No. 46-11;
Matches 41; Conservatio 0; Mismatches 0; Gaps 0.

QY 17 ATTGAGTTGCTAGCTGCGGCTGCGATGCTTTCGCC 57
|||||
DB 61 ATTGAGTTGCTAGCTGCGGCTGCGATGCTTTCGCC 101

RESULT 14
ID AA057191
AC AA057191 standard; mRNA; 27 BP.
XX
XX
DT 26-JUL-1994 (first entry)
XX
XX
DE Enzymatic RNA molecule IL 5 mRNA target sequence.
XX
XX
KW Interferon 5; specificity; clone type; targeted RNA; protein;
KW expression; inhibitor; inhibition; ribozyme; treatment; prophylaxis;
KW prevention; psoriasis; asthma; inflammatory diseases; rickettsiosis;
KW cardiovascular condition; hypertension; arthritis; ss.
XX
XX
OS Synthetic.

XX
XX
FN W09402595-A.
XX
XX
PD 03-FEB-1994.
XX
XX
PE 02-JUL-1993; 93WO-US06316.
XX
XX
PR 17-JUL-1992; 92US-0916763.
XX
XX
PR 07-DEC-1992; 92US-0987132.
XX
XX
PR 07-DEC-1992; 92US-0989848.
XX
XX
PR 07-DEC-1992; 92US-0989849.
XX
XX
PR 19-JAN-1993; 93US-0008895.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX
PI Draper KS, Sullivan SM;
XX
XX
DR WPI: 1994-044851/06.
XX
XX
PE Enzymatic RNA molecules which cleave mRNA used to treat or
PT prevent inflammatory, arthritis, stenosis or cardiovascular diseases
PT or conditions
XX
XX
PS Claim 3; Page 17; 65pp; English.
XX
XX
CC This is an IL-5 mRNA target sequence (nucleotide no. 61) of an
CC enzymatic RNA molecule (ribozyme) which cleaves mRNA associated with
CC the development or maintenance of a portal or asthmatic condition.
CC The concn. of the ribozyme necessary to effect a therapeutic treatment
CC is lower than that of an antisense oligonucleotide and the specificity
CC of action is higher.
XX
XX
SQ Sequence 27 BP; 4 A; 4 C; 8 G; 11 T; 0 other.

Query Match: 51.9%, Score 20, Len 27, Length 27;
Best local Similarity: 100.0%; Pred. No. 0.28;
Matches 22; Conservatio 0; Mismatches 2; Gaps 0.

QY 17 ATTGAGTTGCTAGCTGCGGCTGCG 38
|||||
DB 1 ATTGAGTTGCTAGCTGCGGCTGCG 22

RESULT 14
ID AAX54641/c
AC AAX54641 standard; DNA; 89 BP.
XX
XX
DT 05-JUL-1999 (first entry)
XX
XX
DE Human IL-5 antisense oligonucleotide fragment.
XX
XX
KW Antisense oligonucleotide; multiple target; antisense treatment;
KW hepatic respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.
XX
XX
OS Synthetic.
XX
XX
FN W09913886-A1.
XX
XX
DT 27-MAR-1999.
XX
XX
PR 17-SEP-1998; 98WO 09519419.
XX
XX
PR 09-JUN-1998; 98US-0093972.

PK 17 SEP-1997: 9705 0059160.
 XX
 XX (UNREF.) UNIV EAST CAROLINA.
 XX
 XX NYCC JW.
 XX
 XX W01: 1999-229400219.
 XX
 XX New antisense oligonucleotides used in treatment of, e.g., pulmonary
 PT vasoconstriction
 XX
 PS Disclosure: Page 49: 120pp; English.
 XX
 CC The specification describes various antisense oligonucleotides (AAV2859 X55271)
 CC directed against at least 2 mRNAs selected from target genes, coding and
 CC non-coding regions of mRNAs corresponding to target genes, gene
 CC initiation regions, genomic flanking regions, intron-exon borders, the
 CC 5'-end, the 3'-end and the junction between coding and non-coding
 CC regions and all segments of mRNAs encoding proteins associated with one
 CC or more diseases, conditions or mixtures. The antisense oligonucleotides
 CC may be derived from sequences AAV5272-71. These multiple target
 CC oligonucleotides (specifically AAV5180-271) can be used for the
 CC antisense treatment of diseases and conditions. Typical diseases and
 CC conditions are those associated with impaired respiration and
 CC inflammation, including lung diseases, pulmonary vasoconstriction,
 CC inflammation, allergic rhinitis, acute asthma, allergic asthma, impaired
 CC respiration, respiratory distress syndrome, pain, cystic fibrosis,
 CC pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic
 CC obstructive pulmonary disease (COPD), and chronic bronchitis,
 CC lymphomas, carcinomas, e.g., colon cancer, breast cancer, lung cancer,
 CC pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma,
 CC hepatic metastases as well as all types of cancers which may metastasize
 CC or have metastasized to the lungs, including breast and prostate cancer.
 CC
 SO Sequence 89 BP; 25 A; 20 C; 25 G; 18 T; 1 other;
 Query Match 5.5%; Score 22; DB 20; Length 83;
 Best Local Similarity 100.0%; Prod. No. 0.29;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 YY 17 ATTGAGTTTCAGTCTTTGG 48
 DB 61 ATTGAGTTTCAGTCTTTGG 40
 RESULT 15.
 AAF20210/c
 ID AAF20210 standard; UMA; 89 BP.
 XX
 XX AAF20210;
 XX
 XX 14-MAR-2001 (first entry)
 XX
 XX Human H15 polynucleotide fragment #1777.
 DE
 KW low adenosine and/or sense oligonucleotide; phosphorothioate; allergy;
 KW human airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilation; anti-inflammation;
 KW immunosuppressive; analgesic; hypotensive; cytoprotective;
 KW respiratory obstruction; pulmonary obstruction; impaired respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; FDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; SS.
 XX
 XX Homo sapiens.
 XX
 XX W0200062736-A2.
 XX
 XX 26-OCT-2000.
 XX
 XX 24-MAR-2000; Z000W0-US00020.
 PF

XX
 XX 06-APR-1999: 9905 127150.
 XX
 XX (UNREF.) UNIV EAST CAROLINA.
 XX
 XX (UNREF.) NYCC JW.
 XX
 XX NYCC JW.
 XX
 XX W01: 2000-679539/66.
 XX
 XX
 PT low adenosine (A) content antisense oligonucleotide
 PT trigger adenosine receptor and/or metabolic pathway
 PT cancers and respiratory distress syndromes
 XX
 PS Claim 14: Page 206: 179-pp; English.
 XX
 CC The present invention describes low adenosine (A)
 CC oligonucleotides and compositions (1) comprising
 CC oligonucleotides the A is replaced by a "Universal
 CC (U) can have respiratory bronchodilator, anti-in
 CC immunosuppressive, analgesic, hypotensive, and
 CC The antisense oligonucleotides and (1) can be use
 CC expression and/or activity of target polypeptides
 CC lung/respiratory disorders and mixtures, such
 CC activating peptide receptors and transmitters, the
 CC immunoglobulins and antibodies, and body recep
 CC chemokines, endonuclease, endonuclease specific and to
 CC binding proteins, adhesion molecules and their re
 CC blocking receptors, adhesion receptors, TRAK,
 CC nervous system (NS) and peripheral nervous and
 CC receptors, CNS and peripheral nervous and non
 CC transmitters, neurotransmitters with receptors, as
 CC receptors, binding proteins, and mitogenic assoc
 CC and/or sense oligonucleotides may be used in "thera
 CC including respiratory obstruction (especially for
 CC and/or surfactant hypoproduction) and/or lung infla
 CC condition selected from pulmonary vasoconstriction
 CC allergies, asthma, impaired respiration, respira
 CC (KDS), pain, cystic fibrosis (CF), allergic rhin
 CC hypotension, emphysema, and acute obstructive pul
 CC pulmonary transplantation rejection, pulmonary in
 CC and/or cancer. AAF20210/c AAF20210/c AAF20210/c
 CC fragments and antisense oligonucleotides used in
 CC the present invention.
 XX
 XX Sequence 89 BP; 25 A; 20 C; 25 G; 18 T; 1 other;
 Query Match 5.5%; Score 22; DB 20; Length 83;
 Best Local Similarity 100.0%; Prod. No. 0.29;
 Matches 22; Conservative 0; Mismatches 0;
 YY 17 ATTGAGTTTCAGTCTTTGG 48
 DB 61 ATTGAGTTTCAGTCTTTGG 40
 Search completed November 8, 2002 12:42
 Job time: 106.544 secs



Matches 12: Conservative 10: Mismatches 0: Indels 0: Gaps 0:

QY 17 ATTGACCTTCGAGCTCTGG 48
 DB 1 AAGGACGAGGCGAGGCGGCGG 22

RESULT 2
 US 09 466-852-2/3

Sequence 2: Application US/09466852

Patent No. 668196

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: A SINGLE STEP PURIFICATION OF

TITLE OF INVENTION: RECOMBINANT HUMAN INTERFERON 5

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: MOTOR & CO., INC.

STREET: 126 East Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: USA

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 4.5 IN. 1.44B

COMPUTER: Apple Macintosh

OPERATING SYSTEM: System 7.0.1

SOFTWARE: Microsoft Word 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09 466,852

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: PATENT, GUTTS &

REGISTRATION NUMBER: 33,752

REFERENCE: 21-SEP-1989 33,752

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3195

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 47 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US 09 466-852-2

Query Match 5.5% Score 22 DB 12 Length 47

Best Local Similarity 100.0% Prod. No. 0.099

Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 17 ATTGACCTTCGAGCTCTGG 48
 DB 29 ATTGACCTTCGAGCTCTGG 8

RESULT 4
 US 09 079-849-2

Sequence 2: Application US/09079849

Patent No. 604725

GENERAL INFORMATION:

APPLICANT: Wolfman, Joel K.

APPLICANT: Kallim, Atab S.

TITLE OF INVENTION: IDENTIFICATION OF POLYMERIZATION INFLUENTIATION

FILE REFERENCE: 0998/000091

CURRENT APPLICATION NUMBER: US/09 079,849

CURRENT FILING DATE: 1998-05-15

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO: 2

LENGTH: 316

TYPE: DNA

ORGANISM: Homo sapiens

US-09-079-839-2

Query Match 5.5% Score 22 DB 42 Length 816

Best Local Similarity 100.0% Prod. No. 0.091

Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 17 ATTGACCTTCGAGCTCTGG 48
 DB 61 ATTGACCTTCGAGCTCTGG 82

RESULT 4
 US 09 280-799-78

Sequence 78: Application US/09280799

Patent No. 616603

GENERAL INFORMATION:

APPLICANT: Dohan, Nicholas M.

APPLICANT: Karpas, James G.

APPLICANT: McKay, Robert

TITLE OF INVENTION: ANTISENSE MODULATOR OF INTERFERON 5 SIGNAL

TITLE OF INVENTION: TRANSDUCTION

FILE REFERENCE: ISPI-0340

CURRENT APPLICATION NUMBER: US/09 280,799

CURRENT FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 208

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO: 78

LENGTH: 4230

TYPE: DNA

ORGANISM: Homo sapiens

US 09 280-799-78

Query Match 5.5% Score 22 DB 42 Length 4230

Best Local Similarity 100.0% Prod. No. 0.089

Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 17 ATTGACCTTCGAGCTCTGG 48
 DB 569 ATTGACCTTCGAGCTCTGG 590

RESULT 5
 5424640-1

Patent No. 5424640

APPLICANT: Banaji, Tasuku; Jankovic, Kiyoshi; Socolinsky, Eva

TITLE OF INVENTION: HUMAN B CELL DIFFERENTIATION FACTOR AND

PROTEIN OF PROMOTING SAID FACTOR

NUMBER OF SEQUENCES: 2

CURRENT APPLICATION DATA:

APPLICANT'S REFERENCE: 02-07-79,467

FILING DATE: 21-SEP-1987

SEQ ID NO: 1

LENGTH: 4240

5424640-1

Query Match 5.5% Score 22 DB 62 Length 4240

Best Local Similarity 100.0% Prod. No. 0.099

Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 17 ATTGACCTTCGAGCTCTGG 48
 DB 569 ATTGACCTTCGAGCTCTGG 590

RESULT 6
 US-09-180-864-1

Sequence 1: Application US/09180864

Patent No. 646561b

GENERAL INFORMATION:

APPLICANT: Lopez, Angel

APPLICANT: Vadas, Matthew

APPLICANT: Shannon, Frances


```

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: MOTOR & CO., INC.
CITY: NEW JERSEY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 IN., 1.44B
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/416,962
FILING DATE:
CLASSIFICATION: 424
ATTORNEY: THE W. BAKER
NAME: James, Neil C.
REGISTRATION NUMBER: 33,752
REFERENCE/SEQUENCE NUMBER: 19451A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3199
TELEFAX: (908)594-4720
INVENTOR FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 bases
TYPE: nucleic acid
STRANDNESS: single
POPULACY: linear
US-08-466 B52.1

Query Match: 4.2%, Score 17, DB 1, Length 39
Best Local Similarity: 100.0%, Prod. No. 26,
Matches: 17, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

```

```

US-09-428-111-665
RESULT 10
US-09-428-111-665
Sequence 666, Application US/09/428,111
Patent No. 6,262,334
GENERAL INFORMATION:
APPLICANT: Indigo, Wilson O.
APPLICANT: Steinhilber, Kathleen E.
APPLICANT: Astley, Joe E.
APPLICANT: Burgess, Christopher A.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll, J. Eddie
APPLICANT: Carino, Theodore J.
APPLICANT: Corti, Adam
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NEWLY HUMAN JINX AND GENE EXHIBITION
FILE REFERENCE: CDD-257 (US)
CURRENT APPLICATION NUMBER: US/09/428,111
PRIORITY APPLICATION NUMBER: US 60/298,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 650
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 666
LENGTH: 449
TYPE: DNA
ORGANISM: Homo sapiens
US-09-428-111-666

```

```

Query Match: 4.2%, Score 17, DB 4, Length 449
Best Local Similarity: 100.0%, Prod. No. 27,
Matches: 17, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

```

```

US-09-280-116-171
RESULT 11
US-09-280-116-171
Sequence 171, Application US/09/280,116A
Patent No. 6,314,277
GENERAL INFORMATION:
APPLICANT: Kodison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: US 60/280,116A
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentLynx Ver. 2.0
SEQ ID NO 171
LENGTH: 828
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Proly, oligopeptides
US-09-280-116-171

Query Match: 4.2%, Score 17, DB 4, Length 828
Best Local Similarity: 100.0%, Prod. No. 26,
Matches: 17, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

```

```

US-09-869-147-176
RESULT 12
US-09-869-147-176
Sequence 1, Application US/09/869,176
Patent No. 5,856,157
GENERAL INFORMATION:
APPLICANT: S-0-0-0-0, David
APPLICANT: Gray, Richard
APPLICANT: Medford, June L.
APPLICANT: Munna, R.O.
APPLICANT: Cox-Potter, Diana L.
TITLE OF INVENTION: A Recombinant Acid Phosphatase and Gene Therefor
FILE OF INVENTION: A Recombinant Acid Phosphatase and Gene Therefor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: The Webb Law Firm
STREET: 709 Koppers Building, 436 Seventh Avenue
CITY: Pittsburgh
STATE: PA
COUNTRY: USA
ZIP: 15219-1818
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/869,176
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/018,957
FILING DATE: 04-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Johnson, Barbara E

```


INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 34063
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-09-453-702H-96

Query Match 4.28; Score 17; DB 4; Length 34063;
Best Local Similarity 100.08; Pred. No. 25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 170 AIAAAATGACCACTG 186
|||||
DB 32333 AIAAAATGACCACTG 32349

Search completed: November 8, 2002, 06:10:51
Job Time : 28.0667 secs

Genore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

0M nucleotide - nucleotide search, using SW model

Run on: November 7, 2002, 16:52:17 : Search time 745.2 Seconds
(without alignments)
8746.696 Million cell updates/sec

Title: US-09-755-633-7

Percent score: 402
Sequence: 1 atggagatgcttctgatttt cggatgcttctgctgctgctt 402

Scoring table: dd102-M02
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database:

EST:
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2: cm_ostba:
3: cm_ostba:
4: cm_ostba:
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	20	5.0	305	9	AT666365
2	29	5.0	349	9	AT666525
3	20	5.0	378	17	AQ134641
4	20	5.0	393	17	BH056804
5	20	5.0	417	14	B0456047
6	20	5.0	431	9	AA200961

C	7	20	5.0	305	9	AT666365
C	8	20	5.0	349	9	AT666525
C	9	20	5.0	378	17	AQ134641
C	10	20	5.0	393	17	BH056804
C	11	20	5.0	417	14	B0456047
C	12	20	5.0	431	9	AA200961
C	13	20	5.0	445	9	AA200961
C	14	20	5.0	459	9	AA200961
C	15	20	5.0	473	9	AA200961
C	16	20	5.0	487	9	AA200961
C	17	20	5.0	501	9	AA200961
C	18	20	5.0	515	9	AA200961
C	19	20	5.0	529	9	AA200961
C	20	20	5.0	543	9	AA200961
C	21	20	5.0	557	9	AA200961
C	22	20	5.0	571	9	AA200961
C	23	20	5.0	585	9	AA200961
C	24	20	5.0	599	9	AA200961
C	25	20	5.0	613	9	AA200961
C	26	20	5.0	627	9	AA200961
C	27	20	5.0	641	9	AA200961
C	28	20	5.0	655	9	AA200961
C	29	20	5.0	669	9	AA200961
C	30	20	5.0	683	9	AA200961
C	31	20	5.0	697	9	AA200961
C	32	20	5.0	711	9	AA200961
C	33	20	5.0	725	9	AA200961
C	34	20	5.0	739	9	AA200961
C	35	20	5.0	753	9	AA200961
C	36	20	5.0	767	9	AA200961
C	37	20	5.0	781	9	AA200961
C	38	20	5.0	795	9	AA200961
C	39	20	5.0	809	9	AA200961
C	40	20	5.0	823	9	AA200961
C	41	20	5.0	837	9	AA200961
C	42	20	5.0	851	9	AA200961
C	43	20	5.0	865	9	AA200961
C	44	20	5.0	879	9	AA200961
C	45	20	5.0	893	9	AA200961

ALIGNMENTS

RESULT 1
LOCUS: AT666365
DEFINITION: m12507.x1 (us-09-755-633-7) M18 MUSCULUS
ACCESSION: AT666365
VERSION: 1
KEYWORDS: EST
SOURCE: house mouse
ORGANISM: Mus musculus

REFERENCE
1 (Bases 1 to 305)
Mammalian Genome Project
National Cancer Institute, Human Genome
Tumor Gene Index
Unpublished (1993)
Contact: Robert S. Hershfield, Ph.D.
Email: rshersh@nci.nih.gov

COMMENT
This clone is a member of the highly repetitive
IMAGe Consortium (http://imgc.nci.nih.gov) 1 to
This clone was previously sequenced on the
data is from the 1 to 305
High quality sequence at 294.

FEATURES
Source: /cc/mouse/M18_musculus
Accession: M18_musculus
/db/est/100961

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Molesteomii;
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 393)
AUTHORS Zhao, S., Nierman, W., Malik, J., Shatsman, S., Alizadeh, B., Levin, M.,
Issigoye, G., Geor, K., Kroll, M., Shvartsbeyn, A., Gheorghe, G., P.,
Russell, D., de Jong, P., and Fraser, C. M.
TITLE Mouse HAC End Sequences from library RPOC-24
JOURNAL Unpublished (1999)
COMMENT Other_GSSS: RPOC124-190E14.TJ
Contact: Shanying Zhao
Department of Eukaryotic Genomics
The Institute for Genome Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse PAC library RPOC-24. For PAC
library availability, please contact either de Jong
(pdejong@tigr.org) or Shvartsbeyn (shvartsbeyn@tigr.org). For PAC
resources (http://www.tigr.org/Database/DBHomePage.html), PAC end
sequences (http://www.tigr.org/Database/DBHomePage.html), PAC end
plates (380 rows: 5 columns: 14
Seq primer: 77
Class: BAC ends.
Location/Qualifiers
1..393
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPOC-24-380E14"
/clone_11b="RPOC-24"
/sex="Male"
/cell_type="Epithelial/Brain"
/note="Vector: pIRABAC1; Site_1: BamHI; Site_2: BamHI;
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library was cloned in the pIRABAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA.
BASE COUNT 124 a 89 c 85 g 95 t
ORIGIN
Query Match 5.0%; Score 20; DB 17; Length 393;
Host Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
UY 11 TTCTGCAATTGACTTGTCTA 30
|||||
db 29c TTCTGCAATTGACTTGTCTA 27c
RESULT 5
R0456087 417 bp mRNA linear EST 29 MAY 2002
LOCUS R0456087.1
DEFINITION R0456087.1 mRNA sequence.
ACCESSION R0456087
VERSION R0456087.1 GI:21254959
KEYWORDS EST.
SOURCE Dirofilaria immitis.
ORGANISM Dirofilaria immitis.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Dirofilaria.
REFERENCE 1 (bases 1 to 417)
AUTHORS McCarter, J., Clifton, S., Chapell, B., Page, D., Martindale, J., Wille, T.,
Dante, M., Maria, M., Hillier, L., Kuznetsov, T., Phillips, B., Rogers, Y.,
Cibben, M., Pitter, E., Bennett, J., Franklin, C., Tsagaris, P., R.,
Parker, I., Kennedy, S., Kapitein, L., Ray, C., Galloway, S., P.,
M., Allen, M., Person, B., Swaffler, T., Harvey, N., Sherry, R., Kohn, S.,
Shin, T., Jackson, T., Cardenas, M., McCann, R., Waterston, R., and
Wilson, R.
TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)

COMMENT The Washington Univ. Nematode EST Project,
Washington University School of Medicine,
444 Forest Park, Parkway, Box 8501, St. Louis,
Missouri 63110
Tel: 314 286 1800
Fax: 314 286 1810
Email: estw@wustl.edu
The library was constructed by Claire Mott
at Washington University, St. Louis, MO,
from infected eggs by Dr. Prem Anand from
University, Kari, MO, (Prem Anand, Dr.
University, Kari, MO, (Prem Anand, Dr.
isolated by Dr. Prem Anand from Divergence,
sequencing by Washington University (univ)
Seq primer: 400p from Divergence
High quality sequence: 466.
Location/Qualifiers
1..417
/organism="Dirofilaria immitis"
/strain="R0456087"
/clone_11b="Dirofilaria immitis a
/sex="Male"
/note="Vector: pIRABAC1; Site_1: BamHI; Site_2: BamHI;
RPOC-24 Mouse PAC library produced by Fieret de Jong. The
library was cloned in the pIRABAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA.
BASE COUNT 133 a 85 c 85 g 139 t
ORIGIN
Query Match 5.0%; Score 20; DB 17; Length 417;
Host Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
UY 10 CTCTGCAATTGACTTGTCTA 24
|||||
db 113 CTCTGCAATTGACTTGTCTA 94
RESULT 6
AA200961 431 bp mRNA linear EST 29 MAY 2002
LOCUS AA200961.1
DEFINITION AA200961.1 mRNA sequence.
ACCESSION AA200961
VERSION AA200961.1 GI:21254959
KEYWORDS EST.
SOURCE Dirofilaria immitis.
ORGANISM Dirofilaria immitis.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Dirofilaria.
REFERENCE 1 (bases 1 to 431)
AUTHORS McCarter, J., Clifton, S., Chapell, B., Page, D., Martindale, J., Wille, T.,
Dante, M., Maria, M., Hillier, L., Kuznetsov, T., Phillips, B., Rogers, Y.,
Cibben, M., Pitter, E., Bennett, J., Franklin, C., Tsagaris, P., R.,
Parker, I., Kennedy, S., Kapitein, L., Ray, C., Galloway, S., P.,
M., Allen, M., Person, B., Swaffler, T., Harvey, N., Sherry, R., Kohn, S.,
Shin, T., Jackson, T., Cardenas, M., McCann, R., Waterston, R., and
Wilson, R.
TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: Maria Mott, estw@wustl.edu
Washington University School of Medicine,
444 Forest Park, Parkway, Box 8501, St. Louis,
Missouri 63110
Tel: 314 286 1800
Fax: 314 286 1810
Email: estw@wustl.edu
This clone is available royalty-free through

1.371: double-stranded cDNA was ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pMT3 vector.
RNA provided by Dr. Mounir Bou, Wayne State Univ. Library
constructed and normalized by Bertie Soares and M. Fatima
Honald.

BASE COUNT 168 a 114 c 121 g 135 t

Query Match 5.0% Score 20; DB %; Length 518;

Best Local Similarity: 100.0% Ident. No. 1,556,027

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

RESULT 9

AZ266075 557 bp DNA Insert GSS 26 Jun 2000

LOCUS P01-23-154P16-21 bpct 22 Mus musculus protein from P01-23-154P16

DEFINITION DNA sequence.

ACCESSION AZ266075

VERSION AZ266075.1 GI:9478787

KEYWORDS GSS

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Mammalia; Rodentia; Sciurognathi; Muridae; Mus.

AUTHORS 1 (bases 1 to 557)

1 (bases 1 to 557)

1 (bases 1 to 557)

1 (bases 1 to 557)

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1 (bases 1 to 557)

1 (bases 1 to 557)

Best Local Similarity: 100.0% Ident. No. 1,556,027

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Query Match 5.0% Score 20; DB %; Length 518;

Best Local Similarity: 100.0% Ident. No. 1,556,027

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

RESULT 10

A1645939 576 bp cDNA

LOCUS P01-23-154P16-21 bpct 22 Mus musculus

DEFINITION DNA sequence.

ACCESSION A1645939

VERSION A1645939.1 GI:4724414

KEYWORDS EST

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Mammalia; Rodentia; Sciurognathi; Muridae; Mus.

AUTHORS 1 (bases 1 to 576)

1 (bases 1 to 576)

1 (bases 1 to 576)

1 (bases 1 to 576)

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1 (bases 1 to 576)

1 (bases 1 to 576)

VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mammalia: Eukaryota: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Soricimorpha: Muridae: Murinae: Mus: 1 (bases 1 to 643)
 REFERENCE
 AUTHORS
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, J.D., Yada, T., Torokiy, Y., Watanabe, H., and Sakaki, Y.
 TITLE
 JOURNAL
 COMMENT
 Mouse BAC End Sequences from Library Rpec1-24
 Unpublished (1999)
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 401 838 0200
 Fax: 401 838 0208
 Email: shao@fda.gov
 Clones are derived from the mouse BAC library Rpec1-24. BAC library availability: please contact Shaying Zhao (shaying@fda.gov). Clones may be purchased from BACmap Resources (http://www.bacmap.com) or by mail from BACmap and BACmap (http://www.bacmap.com).
 BACmap 380 row: E column: 14
 Seq primer: SP6
 Class: BAC ends.
 Location/Qualifiers
 L_643
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="Rpec1-24-380E14"
 /clone_1kb="Rpec1-24"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /note="Vector: pTARACT; Site: BamHI; Site: 2; BamHI; Rpec1-24 Mouse BAC library produced by Peter de Jong. The library was cloned in the PARACT cloning vector at the BamHI sites using MspI. Partially digested male C57BL/6J DNA."
 BASE COUNT
 ORIGIN
 159 a 144 c 145 g 141 t
 Query Match 5.0% Score 20; PH 17; Length 643;
 Host Local Similarity 100.0%; Pred. No. 1,440,02;
 Matches 20; Consistency 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 TTGAAATTGAGTTGTTA 40
 11 TTTTTTTTTTTTTTTT
 1b 501 TTGAAATTGAGTTGTTA 242
 RESULT 1:
 AC148772/1 68 bp LNA 1100 23 JAN 2002
 DEFINITION
 Pan troglodytes DNA, clone: M43 01106.10, genomic survey
 sequence.
 ACCESSION
 AC148772
 VERSION
 AC148772.1 GI:16678450
 KEYWORDS
 SOURCE
 Pan troglodytes male lymphocytes DNA, clone: M43 01106.10.
 M43 BAC Library clone: M43 01106.10.
 ORGANISM
 Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Pan.
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 REFERENCE
 AUTHORS
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, J.D., Yada, T., Torokiy, Y., Watanabe, H., and Sakaki, Y.
 TITLE
 JOURNAL
 COMMENT
 BAC end sequences of library Rpec1-43
 Unpublished
 2 (bases 1 to 683)

AUTHORS
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, J.D., Yada, T., Torokiy, Y., Watanabe, H., and Sakaki, Y.
 TITLE
 JOURNAL
 COMMENT
 BAC end sequences of library Rpec1-43
 Unpublished
 2 (bases 1 to 683)
 Clones are derived from the chimpanzee BAC library Rpec1-43. BAC end was generated during the BAC process and may have higher chance of clone tracking errors.
 PRIMERS
 Sequencing: T1
 LIBRARY
 Vector : pTARACT
 K.Site 1 : Rpec1
 R.Site 2 : Rpec1
 Location/Qualifiers
 1 683
 /organism="Pan troglodytes"
 /db_xref="taxon:9698"
 /clone="Rpec1-43-01106.10"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pTARACT; Site: 1; Rpec1; Site: 2; Rpec1; Rpec1-43 Chimpanzee BAC library produced by Peter de Jong. The library was cloned in the PARACT cloning vector at the BamHI sites using MspI. Partially digested male C57BL/6J DNA."
 BASE COUNT
 ORIGIN
 208 a 160 c 150 g 198 t
 Query Match 5.0% Score 20; PH 17; Length 683;
 Host Local Similarity 100.0%; Pred. No. 1,440,02;
 Matches 20; Consistency 0; Mismatches 0; Indels 0; Gaps 0;
 QY 110 ATGGACCTGATGATTCCT 159
 11 TTTTTTTTTTTTTTTTTT
 1b 417 ATGGACCTGATGATTCCT 298
 RESULT 1:
 CH23232M 1014 bp LNA 1100 15 MAY 2000
 DEFINITION
 Tetraodon nigroviridis genome survey sequence 17 end of clone
 015117 of library G from Tetraodon nigroviridis, genomic survey
 sequence.
 ACCESSION
 AL238063
 VERSION
 AL238063.1 GI:7897198
 KEYWORDS
 SOURCE
 ORGANISM
 Tetraodon nigroviridis.
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 Actinopterygii: Neopterygii: Teleostei: Euteleostei: Neoteleostei:
 Acanthomorpha: Acanthopterygii: Perciformes: Tetraodontiformes:
 Tetraodontidae: Tetraodon.
 1 (bases 1 to 1013)
 REFERENCE
 Hest, C., Collins, H., Jallou, O., Bastiva, C., Boune, L., Fisher, A.,
 Hest, A., Frazee, C., Winkler, P., Brothier, P., Guillet, F.,
 Smith, W., and Weissenbach, J.
 Human genome: estimate of the 2.8-3.4 Gb genome size analysis using
 tetraodon nigroviridis DNA sequence.
 Unpublished
 2 (bases 1 to 1013)
 REFERENCE
 Hest, C., Collins, H., Jallou, O., Bastiva, C., Frazee, C., Fisher, A.,
 Boune, L., Hest, A., Guillet, F., Smith, W., Hest, A., and
 Weissenbach, J.
 Characterization and repeat analysis of the repeat genome of the
 freshwater pufferfish Tetraodon nigroviridis
 Unpublished
 3 (bases 1 to 1013)
 REFERENCE
 Hest, C., Collins, H., Jallou, O., Bastiva, C., Frazee, C., Fisher, A.,
 Boune, L., Hest, A., Guillet, F., Smith, W., Hest, A., and
 Weissenbach, J.
 Characterization and repeat analysis of the repeat genome of the
 freshwater pufferfish Tetraodon nigroviridis
 Unpublished
 3 (bases 1 to 1013)
 REFERENCE
 Hest, C., Collins, H., Jallou, O., Bastiva, C., Frazee, C., Fisher, A.,
 Boune, L., Hest, A., Guillet, F., Smith, W., Hest, A., and
 Weissenbach, J.
 Characterization and repeat analysis of the repeat genome of the
 freshwater pufferfish Tetraodon nigroviridis
 Unpublished
 3 (bases 1 to 1013)

http://www.genoscope.cns.fr/tetradon.

FEATURES

Location/Qualifiers

1..1013

/db_xref="taxon:95885"

/dbname="95885"

/db_xref="genbank:U01517"

BASE COUNT

303 A 190 C 242 G 226 T 2 others

ORIGIN

Query Match

Best Local Similarity 100.0%, Prod. No. 1.2e+02,

Matches 29, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY

313 TGTGACGACACATGATGAC 332

DB

658 TGTGACGACACATGATGAC 677

RESULT 14

ACCESSION

AF205009.1 21:9399929

VERSION

AF205009.1 21:9399929

SOURCE

AF205009.1 21:9399929

ORGANISM

AF205009.1 21:9399929

REFERENCE

AF205009.1 21:9399929

AUTHORS

AF205009.1 21:9399929

TITLE

AF205009.1 21:9399929

JOURNAL

AF205009.1 21:9399929

COMMENT

AF205009.1 21:9399929

FEATURES

AF205009.1 21:9399929

SOURCE

AF205009.1 21:9399929

BASE COUNT

AF205009.1 21:9399929

ORIGIN

AF205009.1 21:9399929

QUERY MATCH

AF205009.1 21:9399929

BEST LOCAL SIMILARITY

AF205009.1 21:9399929

MATCHES

AF205009.1 21:9399929

CONSERVATIVE

AF205009.1 21:9399929

MISMATCHES

AF205009.1 21:9399929

INDELS

AF205009.1 21:9399929

GAPS

AF205009.1 21:9399929

OTHERS

AF205009.1 21:9399929

RESULTS

AF205009.1 21:9399929

LOCUS

AF205009.1 21:9399929

DEFINITION

AF205009.1 21:9399929

ACCESSION

AF205009.1 21:9399929

VERSION

AF205009.1 21:9399929

SOURCE

AF205009.1 21:9399929

ORGANISM

AF205009.1 21:9399929

TITLE

AF205009.1 21:9399929

JOURNAL

AF205009.1 21:9399929

COMMENT

AF205009.1 21:9399929

FEATURES

AF205009.1 21:9399929

RESULT 15

LOCUS

AV256645.1 297 bp mRNA

DEFINITION

AV256645.1 297 bp mRNA

ACCESSION

AV256645.1 297 bp mRNA

VERSION

AV256645.1 297 bp mRNA

SOURCE

AV256645.1 297 bp mRNA

ORGANISM

AV256645.1 297 bp mRNA

TITLE

AV256645.1 297 bp mRNA

JOURNAL

AV256645.1 297 bp mRNA

COMMENT

AV256645.1 297 bp mRNA

FEATURES

AV256645.1 297 bp mRNA

SOURCE

AV256645.1 297 bp mRNA

BASE COUNT

AV256645.1 297 bp mRNA

ORIGIN

AV256645.1 297 bp mRNA

QUERY MATCH

AV256645.1 297 bp mRNA

BEST LOCAL SIMILARITY

AV256645.1 297 bp mRNA

MATCHES

AV256645.1 297 bp mRNA

CONSERVATIVE

AV256645.1 297 bp mRNA

MISMATCHES

AV256645.1 297 bp mRNA

INDELS

AV256645.1 297 bp mRNA

GAPS

AV256645.1 297 bp mRNA

OTHERS

AV256645.1 297 bp mRNA

RESULTS

AV256645.1 297 bp mRNA

LOCUS

AV256645.1 297 bp mRNA

DEFINITION

AV256645.1 297 bp mRNA

ACCESSION

AV256645.1 297 bp mRNA

VERSION

AV256645.1 297 bp mRNA

SOURCE

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ORGANISM

AV256645.1 297 bp mRNA

TITLE

AV256645.1 297 bp mRNA

JOURNAL

AV256645.1 297 bp mRNA

COMMENT

AV256645.1 297 bp mRNA

FEATURES

AV256645.1 297 bp mRNA

SOURCE

AV256645.1 297 bp mRNA

BASE COUNT

AV256645.1 297 bp mRNA

ORIGIN

AV256645.1 297 bp mRNA

QUERY MATCH

AV256645.1 297 bp mRNA

BEST LOCAL SIMILARITY

AV256645.1 297 bp mRNA

MATCHES

AV256645.1 297 bp mRNA

CONSERVATIVE

AV256645.1 297 bp mRNA

MISMATCHES

AV256645.1 297 bp mRNA

INDELS

AV256645.1 297 bp mRNA

GAPS

AV256645.1 297 bp mRNA

OTHERS

AV256645.1 297 bp mRNA

cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence [5'
 GATGAGAGATTCTCCAGTTAAATTAATTAATTTTCCCCCCCC 3']. cDNA
 was cloned into the XhoI and BamHI sites. Vector: a
 modified phuescript KS(+) after bulk excision from Lambda
 Fli I. Cloning sites, 5' end: SalI; 3' end: BamHI."

BASE COUNT 81 a 42 c 57 g 113 t

ORIGIN

Query Match 4.7%; Score 19; DB 9; Length 293;
 Best Local Similarity 100.0%; Pred. No. 5,2c102;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 GACGATTGAGAGACCAAA 232
 |||
 DB 182 GACGATTGAGAGACCAAA 164

Search completed: November 8, 2002, 01:01:46
 Job time : 748.2 secs

Genome version 5.1.3
Copyright (c) 1998 - 2002 CompuLink Ltd.

MM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 08:51:35, Search time: 1140.33 Seconds

(Without alignments)
10550.548 Million cell updates/sec

Title: US-09-755-633-7

Perfect score: 402

Sequence: 1 atgaagatctctctcaatt

Scoring table: IDENTITY NUC

Gapop 10.0 / Gapext 1.0

Searched: 2054640 seqs 1456140478 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listed first 45 summaries

Database: 1: qb_da: 2: qb_da: 3: qb_da: 4: qb_da: 5: qb_da: 6: qb_da: 7: qb_da: 8: qb_da: 9: qb_da: 10: qb_da: 11: qb_da: 12: qb_da: 13: qb_da: 14: qb_da: 15: qb_da: 16: qb_da: 17: qb_da: 18: qb_da: 19: qb_da: 20: qb_da: 21: qb_da: 22: qb_da: 23: qb_da: 24: qb_da: 25: qb_da: 26: qb_da: 27: qb_da: 28: qb_da: 29: qb_da: 30: qb_da: 31: qb_da: 32: qb_da: 33: qb_da: 34: qb_da: 35: qb_da: 36: qb_da: 37: qb_da: 38: qb_da: 39: qb_da: 40: qb_da: 41: qb_da: 42: qb_da: 43: qb_da: 44: qb_da: 45: qb_da:

Score greater than or equal to the score of the
and is derived by analysis of the total score.

SUMMARIES

Result No.	Score	Query Match	Length	Ref	Accession	Source	Organism	Reference	Authors	Title
1	402	100.0	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
2	402	99.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
3	402	98.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
4	402	98.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
5	402	97.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
6	402	97.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
7	402	96.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
8	402	96.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
9	402	95.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
10	402	95.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
11	402	94.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
12	402	94.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
13	402	93.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
14	402	93.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
15	402	92.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
16	402	92.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
17	402	91.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
18	402	91.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
19	402	90.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
20	402	90.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
21	402	89.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
22	402	89.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
23	402	88.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
24	402	88.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
25	402	87.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
26	402	87.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
27	402	86.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
28	402	86.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
29	402	85.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
30	402	85.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
31	402	84.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
32	402	84.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
33	402	83.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
34	402	83.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
35	402	82.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
36	402	82.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
37	402	81.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
38	402	81.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
39	402	80.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
40	402	80.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
41	402	79.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
42	402	79.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
43	402	78.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
44	402	78.2	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression
45	402	77.7	100	4	AF01919	Canis familiaris	Canis familiaris	Yano, S., et al.	Yano, S., et al.	Canine Interleukin-10 (IL-10) gene expression

ALIGNMENTS

RESULT 1
AF01919
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

Journal of Clinical Investigation 106 (4): 471-478 (1999)

MELINE 2 (bases 1 to 454)

REFERENCE 2 (bases 1 to 454)

AUTHORS Harley, R., Day, M.J., Gatelydd-Jones, T.J., Harbour, D.A. and Halls, C.K.

TITLE Direct Submission

JOURNAL Submitted (27-FEB-1998) Clinical Veterinary Science, Bristol University, Langford House, Langford, Wiltshire, Wiltshire, UK

FEATURES

SOURCE

1. 454

ORGANISM "Homo sapiens"

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Db 405 GACCTTCTGGTGAATGAACAGAGTGGATATGAAAGT 446

RESULT 15
HSL15K
100%

DEFINITION Human mRNA for T-cell replacing factor (interleukin-5).
ACCESSION X04684
VERSION 1 (bases 1 to 816)
KEYWORDS interleukin; interleukin-5; signal peptide; T-cell replacing factor.

SOURCE Homo sapiens
ORGANISM Homo sapiens
TAXID 9606
PUBMED 87066782
JOURNAL Nucleic Acids Res. 14 (22): 9149-9158 (1986)
MEDLINE 87066782
PUBMED 87066782
FEATURES
source location/Qualifiers
1..816
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="pHL-5-30"
/coll_line="ATL-2"
/cell_type="T-cell" (of leukemia patients)"
/dev_stage="adult"
45..449
/note="put. precursor polypeptide"
/codon_start=1
/protein_id="CAA28390.1"
/db_xref="GI:33836"
/translation="MEMELSLTAAAYVAIPETSAVLKTLTSLTRILL
LANETIRIPVIRKINHOCTEIEFGCTGFSQTVGGSTVPRFKNSLKKYIDGK
KKGCHRRRVNQFDYLCERPLGVNMTETLES"
45..110
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/product="put. mature polypeptide (AA 1-112)"
183..191
/note="post. N-glycosylation site"
412..420
/note="post. N-glycosylation site"
791..796
/note="put. polyA signal"
816
/note="polyA site"
BASE COUNT 277 a 137 c 164 g 238 t
ORIGIN

Query Match 69.0%; Score 277.2; DB 9; Length 816;
Best local similarity 80.6%; Pred. No. 4,7e-67;
Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Q7 1 ATGAGAAATGCTTCAATTTGAGTTTCTATATCTTGAAGATGATTAAGTACTGACCTT 60
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Db 45 ATGAGATGCTTCTCAATTTGAGTTTCTATATCTTGAAGATGATTAAGTACTGACCTT 104
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Q7 61 GTGTGAGAAATGCCATGAAATGAGCTGGTGGAGAGACCTTGACACTGCTCCACATCAI 120
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Db 105 GCGACAGAAATGCCCAAGATGCAATGATGATGAAGAGACCTTGACACTGCTTCTACTCAT 164
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Q7 121 GCAACTGAGCTATAGCGGATGGAGACCTGATGCTACTCTACTCTGAAAA AAAAATCAC 180
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Db 165 GCAACTGAGCTATAGCGGATGGAGACCTGATGCTACTCTACTCTGAAAA AAAAATCAC 224
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Q7 181 CAAGTGTGATTAATTAATTTTAAAGGTATAGACGATTAAGAGATCAAGTCCCGC 240

Db 225 CAAGTGTGATTAATTAATTTTAAAGGTATAGACGATTAAGAGATCAAGTCCCGC 240
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Q7 241 GCGACAGCTGTGATGAAATGAGCTGGTGGAGAGACCTTGACACTGCTCCACATCAI 280
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Db 285 GCGACAGCTGTGATGAAATGAGCTGGTGGAGAGACCTTGACACTGCTCCACATCAI 324
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Q7 301 CAAGTGTGATTAATTAATTTTAAAGGTATAGACGATTAAGAGATCAAGTCCCGC 340
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Db 345 CAAGTGTGATTAATTAATTTTAAAGGTATAGACGATTAAGAGATCAAGTCCCGC 384
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Q7 361 GATTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 400
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Db 405 GATTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 444
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Search completed: November 7, 2002, 16:4:13
Job time: 1142.33 secs



P1 Stim G, Yang S, Jiroitz M, Wenderling BS
 XX
 XX WPI: 2090-0724/23/06.
 LR P-PSDB: AAV58220.
 XX
 P1 Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 P1 useful for treating or preventing e.g. tumors or autoimmune disease
 XX
 PS Claim (b) Page 226-227; 264pp; English.
 XX
 CC Sequences AAV55546-255551 represent cDNA sequences encoding
 CC canine interleukin 5 (IL-5). The invention relates to canine
 CC IL-4, canine or feline Fli-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interleukin alpha (IFN-alpha) and feline granulocyte colony-stimulating
 CC colony-stimulating factor (GM-CSF), and nucleotides where these
 CC immunoregulatory proteins, the proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumors, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are used as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense
 CC oligonucleotides). The proteins may be used to raise antibodies and to
 CC screen for modulators of activity, while the antibodies may be used in
 CC detection, and in drug targeting.
 CC
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 S0 Sequence 345 BP; 120 A; 68 C; 78 G; 79 T; 0 other:
 Query Match 85.8%, Score 315; 100 21; Length 345;
 Best Local Similarity 100.0%; Prod. No. 110 93;
 Matches 345; Conservative 0; Mismatches 0; Indel: 0; Gaps 0;
 UY 58 TTTCGTAGAAATCCATCAATACATGCTGGTCAAGACCTTGACACTCTCTGCACAT 117
 LB 1 TTTCGTAGAAATCCATCAATACATGCTGGTCAAGACCTTGACACTCTCTGCACAT 117
 UY 118 CATCCAACTGACTGATATAGGCGATGGGAACCTGATGATCTCTACTCTGAAATAAAT 177
 LB 61 CATCCAACTGACTGATATAGGCGATGGGAACCTGATGATCTCTACTCTGAAATAAAT 177
 UY 178 CATCCAACTGACTGATATAGGCGATGGGAACCTGATGATCTCTACTCTGAAATAAAT 227
 LB 121 CATCCAACTGACTGATATAGGCGATGGGAACCTGATGATCTCTACTCTGAAATAAAT 227
 UY 248 CATCCAACTGACTGATATAGGCGATGGGAACCTGATGATCTCTACTCTGAAATAAAT 297
 LB 181 CATCCAACTGACTGATATAGGCGATGGGAACCTGATGATCTCTACTCTGAAATAAAT 297
 UY 298 CATCCAACTGACTGATATAGGCGATGGGAACCTGATGATCTCTACTCTGAAATAAAT 357
 LB 241 CATCCAACTGACTGATATAGGCGATGGGAACCTGATGATCTCTACTCTGAAATAAAT 357
 UY 358 CATCCAACTGACTGATATAGGCGATGGGAACCTGATGATCTCTACTCTGAAATAAAT 402
 LB 401 CATCCAACTGACTGATATAGGCGATGGGAACCTGATGATCTCTACTCTGAAATAAAT 402
 UY 401 CATCCAACTGACTGATATAGGCGATGGGAACCTGATGATCTCTACTCTGAAATAAAT 445
 LB 401 CATCCAACTGACTGATATAGGCGATGGGAACCTGATGATCTCTACTCTGAAATAAAT 445
 RESOUT 7
 AAV55551/7
 ID AAV55551 strand: cDNA; 445 BP;
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 AC AAV55551;
 XX
 DI 14 MAR-2000 (first entry)
 XX
 DE Canine mature interleukin-5 (IL-5) cDNA complement.
 XX
 XX Interleukin-5, IL-5, antibody, canine, inhibitor, immune response,
 KM immunoregulation, tumour, cancer, autoimmune disease, vaccine; 88.

XX
 OS Canis familiaris.
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 XX W09961618-A2.
 PN
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 PD 02-DEC-1999.
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 PF 28-MAY-1999; 998 181114.
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 PR 29-MAY-1998; 9808 181114.
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 PA (HEK-) HESKA CORP.
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 P1 Stim G, Yang S, Jiroitz M, Wenderling BS
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 LR WPI: 2090-0724/23/06.
 LR P-PSDB: AAV58220.
 XX
 PS Claim (b) Page 226; 264pp; English.
 XX
 CC Sequences AAV55546-255551 represent cDNA sequences
 CC canine interleukin 5 (IL-5). The invention relates to canine
 CC IL-4, canine or feline Fli-3 ligand, canine or feline
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interleukin alpha (IFN-alpha) and feline granulocyte colony-stimulating
 CC colony-stimulating factor (GM-CSF), and nucleotides where these
 CC immunoregulatory proteins, the proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
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 CC response in animals (particularly cats, dogs, horses and humans).
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 CC
 XX
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 Best Local Similarity 100.0%; Prod. No. 110 93;
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Fri Nov 8 12:51:37 2002

us-09-755-633-7_1.rng

Page

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Job time : 10.6 secs



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✓

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BASE COUNT 114 a 73 c 71 g 95 t 1 other
 ORIGIN

Query Match

Best Local Similarity 7.58; Score 30; DB 4; Length 354;
 Best Local Similarity 100.08; Prod. No. 2.3e-05;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 TCTATGCTCTTTATTAAACACAGTTT 136
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 ID 264 TCTATGCTCTTTATTAAACACAGTTT 235

RESULT 15

AF294756/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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SALMIRI SCIUREUS

SALMIRI SCIUREUS

SALMIRI SCIUREUS

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Search completed: November 7, 2002, 21:30:48
 Job time : 1141.27 secs



Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 CCAAGAGCTAGCAACTCAAT 386

DB 22 CCAAGAGCTAGCAACTCAAT 1

RESULT 2

US-08-466-852-2

Sequence 2, Application US/09466852

Patent No. 5681936

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: A SINGLE STEP PURIFICATION OF

TITLE OF INVENTION: RECOMBINANT HUMAN INTERLEUKIN 5

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 East Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: USA

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 in, 1.4Kb

COMPUTER: Apple Macintosh

OPERATING SYSTEM: System 7.0.1

SOFTWARE: Microsoft Word 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,852

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Panzer, Curtis C.

REGISTRATION NUMBER: 33,752

REFERENCE/DOCKET NUMBER: 191511A

TELEPHONE: (908)594-3199

TELEFAX: (908)594-4720

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 47 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-466-852-2

Query Match 5.5%; Score 22; DB 1; Length 47;

Best Local Similarity 100.0%; Pred. No. 0.095;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 CCAAGAGCTAGCAACTCAAT 386

DB 8 CCAAGAGCTAGCAACTCAAT 29

RESULT 3

US-09-079-839-2/c

Sequence 2, Application US/09079839

Patent No. 6048726

GENERAL INFORMATION:

APPLICANT: Wellman, Joel K.

TITLE OF INVENTION: INITIATION OF EOSINOPHILIC INFLAMMATION

FILE REFERENCE: 09998/00201

CURRENT APPLICATION NUMBER: 79,079,839, 833

CURRENT FILING DATE: 1998-05-15

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSBY for Windows Version 3.0

SEQ ID NO: 2

LENGTH: 816

TYPE: DNA

ORGANISM: Homo sapiens

US-09-079-839-2

Query Match

Best Local Similarity 100.0%; Pred. No. 0.091;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 CCAAGAGCTAGCAACTCAAT 386

DB 62 CCAAGAGCTAGCAACTCAAT 61

RESULT 4

US-09-280-799-78/c

Sequence 78, Application US/09280799

Patent No. 6136603

GENERAL INFORMATION:

APPLICANT: Dean, Nicholas M.

APPLICANT: McKay, Robert

APPLICANT: Karris, James G.

TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 5 SIGNAL

FILE REFERENCE: ISPH-0340

CURRENT APPLICATION NUMBER: US/09/280,799

CURRENT FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 208

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 78

LENGTH: 3230

TYPE: DNA

ORGANISM: Homo sapiens

US-09-280-799-78

Query Match 5.5%; Score 22; DB 1; Length 3230;

Best Local Similarity 100.0%; Pred. No. 0.089;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 CCAAGAGCTAGCAACTCAAT 386

DB 590 CCAAGAGCTAGCAACTCAAT 569

RESULT 5

US-09-5324640-1/c

Patent No. 5324640

APPLICANT: Hoeft, Tasuku; Taylor, Kiyoshi; Sengen, Eri

PROCESS OF PRODUCING SAID FACTOR

NUMBER OF SEQUENCES: 2

CURRENT APPLICATION DATA:

ALLOCATION NUMBER: 0520731,457

FILING DATE: 21-SEP-1987

SEQ ID NO: 1

LENGTH: 3230

5324640-1

Query Match 5.5%; Score 22; DB 6; Length 3230;

Best Local Similarity 100.0%; Pred. No. 0.089;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 CCAAGAGCTAGCAACTCAAT 386

DB 590 CCAAGAGCTAGCAACTCAAT 569

RESULT 6

US-09-160-804-1/c

Sequence 1, Application US/09180864

Patent No. 6465616

GENERAL INFORMATION:

APPLICANT: Lopez, Angel

APPLICANT: Vadas, Matthew

APPLICANT: Shannon, Frances

APPLICANT: Bastias, Stan
 APPLICANT: Hwy. A1140 W
 TITLE OF INVENTION: AN INTERLEUKIN-5 ANTAGONIST
 FILE REFERENCE: 99722
 CURRENT APPLICATION NUMBER: 07/07180,864
 PRIOR FILING DATE: 1999-04-12
 PRIOR APPLICATION NUMBER: 08/991,438
 PRIOR FILING DATE: 1994-07-28
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: Patented Ver. 2.1
 SEQ ID NO: 1
 LENGTH: 477
 TYPE: DNA
 ORGANISM: nucleotide sequence encoding modified IL-5
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (4)...(366)
 DS-09-180-864-1

Query Match 5.28; Score 21; DB 4; Length 477
 Host Local Similarity 100.0%; Prod. No. 0.29;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Caps 0

QY 213 ACAGAGTGGAGTGGATTTAT 263
 DB 154 TCGACAGTGGAGTGGATTTAT 134

RESULT 7
 SEQ-0994-10957-16
 Sequence 16, Application PG/US9410957
 GENERAL INFORMATION:
 APPLICANT: Goldstone, Harry; Kollman, Tobias R.
 TITLE OF INVENTION: Immunodeficient Mouse Models of
 TITLE OF INVENTION: Pathogenesis of Human Disease and Utility and Toxicity of
 NUMBER OF SEQUENCES: 28
 CLASSIFICATION: 28
 CORRESPONDENCE ADDRESS:
 ADDRESS: Law Office of Spelman and Spelman
 STREET: 418 N Washington Street
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22314
 COMPUTER REAVAILABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 COMPUTER: IBM Clone, 8088 Turbo
 SOFTWARE: Word Perfect, Version 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US 94/10957
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Richard A. Steinberg
 REGISTRATION NUMBER: 26,588
 REFERENCE/KEY NUMBER: PCT-149/GIP 11
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 549-2282
 TELEFAX: (703) 846-0106
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEICAL: no
 ORIGINAL SOURCE:
 ORGANISM: human
 FEATURE:
 NAME/KEY: 3' UTR
 LOCATION: 3' UTR
 DS-0994-10957-16

Query Match 4.74; Score 19; DB 5; Length 477
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 Matches 19; Conservative 0; Mismatches 0

QY 42 CTGAGGAGTGGAGTGGATTTAT 263
 DB 1 CTGAGGAGTGGAGTGGATTTAT 134

RESULT 8

DS-08-621-841-48/c
 Sequence 48, Application PG/US 94/08669
 Patent No. 6096669

GENERAL INFORMATION:

APPLICANT: Stealey, Margaret A.

TITLE OF INVENTION: Interleukin-5 Antagonist

TITLE OF INVENTION: Test Set

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESS: Four Embarcadero, Suite 44

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111

COMPUTER REAVAILABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: Picta 1.0 Release 1.0, Version 1.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/97/07181

FILING DATE: 22 MAR 1997

CLASSIFICATION: 113

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/97 5794.0

FILING DATE: 22 MAR 1994

ATTORNEY/AGENT INFORMATION:

NAME: Dwyer, William H.

REGISTRATION NUMBER: 24,100

REFERENCE/KEY NUMBER: A. 5. 119

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 281-1000

TELEFAX: (415) 408-1240

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

HYPOTHEICAL: NO

DS-08-621-841-48

Query Match

Host Local Similarity 100.0%; Prod. No. 2.94;
 Matches 18; Conservative 0; Mismatches 0

QY 216 ACAGTGGAGTGGATTTAT 263
 DB 21 ACAGTGGAGTGGATTTAT 134

RESULT 9

DS-08-466-852-1/c
 Sequence 1, Application US/0840852
 Patent No. 5681936

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: A SYNTHETIC PEPTIDE N-TERMINAL HUMAN INTERLEUKIN-5

TITLE OF INVENTION: 507-880000 HUMAN INTERLEUKIN-5

```

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: METEC 3000, Inc.
STREET: 126 East Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
COMPUTER: Apple Macintosh
SERIALING SYSTEM: System 7.0.1
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 03,79,16,652
FILING DATE:
CLASSIFICATION: 424
ALTERNATE SEQ ID NO: 1
NAME: Ladd, E. A. Jr.
REGISTRATION NUMBER: 33,752
REFERENCE/WORKER NUMBER: 19451A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-4199
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 bases
TYPE: nucleic acid
STRANDEDNESS: single
POLYMER: linear
MULTIPLE TYPE: DNA (genomic)
US-09-466-852-1

Query Match 4.28; Score 17; DB 1; Length 49;
Host Local Similarity 100.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 AGTATACAACTCAAT 386
DB 49 AGCTATCAAACTCAAT 23

RESULT 10
US-09-428-111-644-7
Sequence 666, Application US/09428111
GENERAL INFORMATION:
APPLICANT: Endrey, Wilson O.
APPLICANT: Steimann, Kathleen E.
APPLICANT: Astley, John H.
APPLICANT: Butress, Christopher A.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll, III, Eddie
APPLICANT: Carino, Theodore J.
APPLICANT: Lucif, Adam
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CDD-257 (US)
CURRENT APPLICATION NUMBER: US/09428111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 66/088,401
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 666
LENGTH: 449
TYPE: DNA
ORGANISM: Homo sapiens
US-09-428-111-646

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Query Match 4.28; Score 17; DB 4; Length 449;
Host Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 TATTATTCACACACCT 158
DB 208 TATTATTCACACACCT 192

RESULT 11
US-09-280-116-171-6
Sequence 171, Application US/09280116A
Patent No. 5431427
GENERAL INFORMATION:
APPLICANT: Robinson, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: None
REGISTRATION NUMBER: 41,696,176,665
CURRENT FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 171
LENGTH: 923
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION: polyA oligonucleotides
US-09-280-116-171

Query Match 4.28; Score 17; DB 4; Length 823;
Host Local Similarity 100.0%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 TTAATTCACACACCTAG 245
DB 697 TTAATTCACACACCTAG 681

RESULT 12
US-08-869-147-1
Sequence 1, Application US/08869147
Patent No. 5856157
GENERAL INFORMATION:
APPLICANT: Schuller, David
APPLICANT: Grady, Richard
APPLICANT: Medford, June L.
APPLICANT: Muma, R.O.
APPLICANT: Cox-Foster, Diana L.
TITLE OF INVENTION: A No. 5856157-1 D1 14:00-ACP Family
TITLE OF INVENTION: Acid Isomerase and Gene Thereof
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: The Webb Law Firm
STREET: 700 Koppers Building, 400 Seventh Avenue
CITY: Pittsburgh
STATE: PA
COUNTRY: USA
ZIP: 15219-1818
FILE REFERENCE: None
COMPUTER READABLE FORM:
COMPUTER: IBM Compatible
SERIALING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09469147
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 66/018,957
FILING DATE: 04 JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Johnson, Barbara E.

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INFORMATION FOR SEQ ID NO: 96:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 34064
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 96:
 US 09 454-7026-96

Query Match: 4.28; Score 17; FR 4; Length 34064;

Best Local Similarity: 100.0%; Ident. No. 25;

Matches: 17; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

US 217 PATENTGATTTTTTAT 233

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DB 42449 CATTGATGATTTTAT 42333

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 Job time: 24.0667 secs

GenCorp version 5.1.4
Copyright (c) 1994 - 2002 GenCorp Ltd.

0M nucleotide - nucleotide search, using SW method

Run on: November 7, 2002, 16:52:17, Search time 745.2 Seconds
(without alignments)
8736.646 Million cell updates/sec

Title: US-09-755-633-B

Feature scores: 402
Sequence: 1 nucleotide alignment,adattcagaagacattctat 402

Scoring table:
Gapop 60.0, Gapext 60.0

Search: 16154066 steps, 8057743376 residues

Word size: 4

Total number of hits satisfying chosen parameters: 32308132

Minimum hit seq length: 0
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Post-processing: Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	20	5.0	14	A0134641
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FEATURES

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DEFINITION
ACCESSION A1666365
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
SOURCE

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2. *Copyright (c) 1994 - 2002 GenCorp Ltd.*
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ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 393)

REFERENCE

Zhao, S., Newman, W., Mink, J., Shusterman, S., Minner, R., Lewis, M.,
Russek, J., de Jong, P., and Fraser, D.M.
Mouse hAT End Sequences from Library Rpt-24
Unpublished (1999)
E-mail address: Rpt-24@EMBL.EMBL

COMMENT

Contact: Shaojun Zhao
Department of Eukaryotic Genomics
The Institute for Genome Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
E-mail: shaojun@igmc.org

Clones are derived from the mouse hAT library Rpt-24. For hAT
library availability, please contact Peter de Jong
(pdejong@igmc.org). Clones may be purchased from hATPAC
Resources (http://www.igmc.org/igmc/igmc.html) or from
Peter de Jong (pdejong@igmc.org).
Plasmid: 3kb, Rpt-24, Rpt-24, Rpt-24, Rpt-24, Rpt-24, Rpt-24
Seq primer: 17
Class: hAT ends.

FEATURES

Source

Location/Qualifiers
1..393

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COMMENT

Contact: McArthur, J.
The Washington State University
Washington State University, Pullman, WA 99164-5010
4444 Forest Park Highway, Box 8501, St. Louis,
Tel: 314 286 1000
Fax: 314 286 1000
E-mail: jmcArthur@washington.edu

FEATURES

Source

Location/Qualifiers
1..417

/organism "Mus musculus"

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/db_xref "GenBank:U00000"

COMMENT

Contact: McArthur, J.
The Washington State University
Washington State University, Pullman, WA 99164-5010
4444 Forest Park Highway, Box 8501, St. Louis,
Tel: 314 286 1000
Fax: 314 286 1000
E-mail: jmcArthur@washington.edu

FEATURES

Source

Location/Qualifiers
1..417

/organism "Mus musculus"

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FEATURES location/qualifiers
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locus "taxon:99888"

locus "11b-6"

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locus "mouse sequence ID: 009001540941 end: 17"

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FEATURES location/qualifiers
source

location "Mammalia/mammals"

locus "taxon:99888"

locus "11b-6"

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locus "mouse sequence ID: 009001540941 end: 17"

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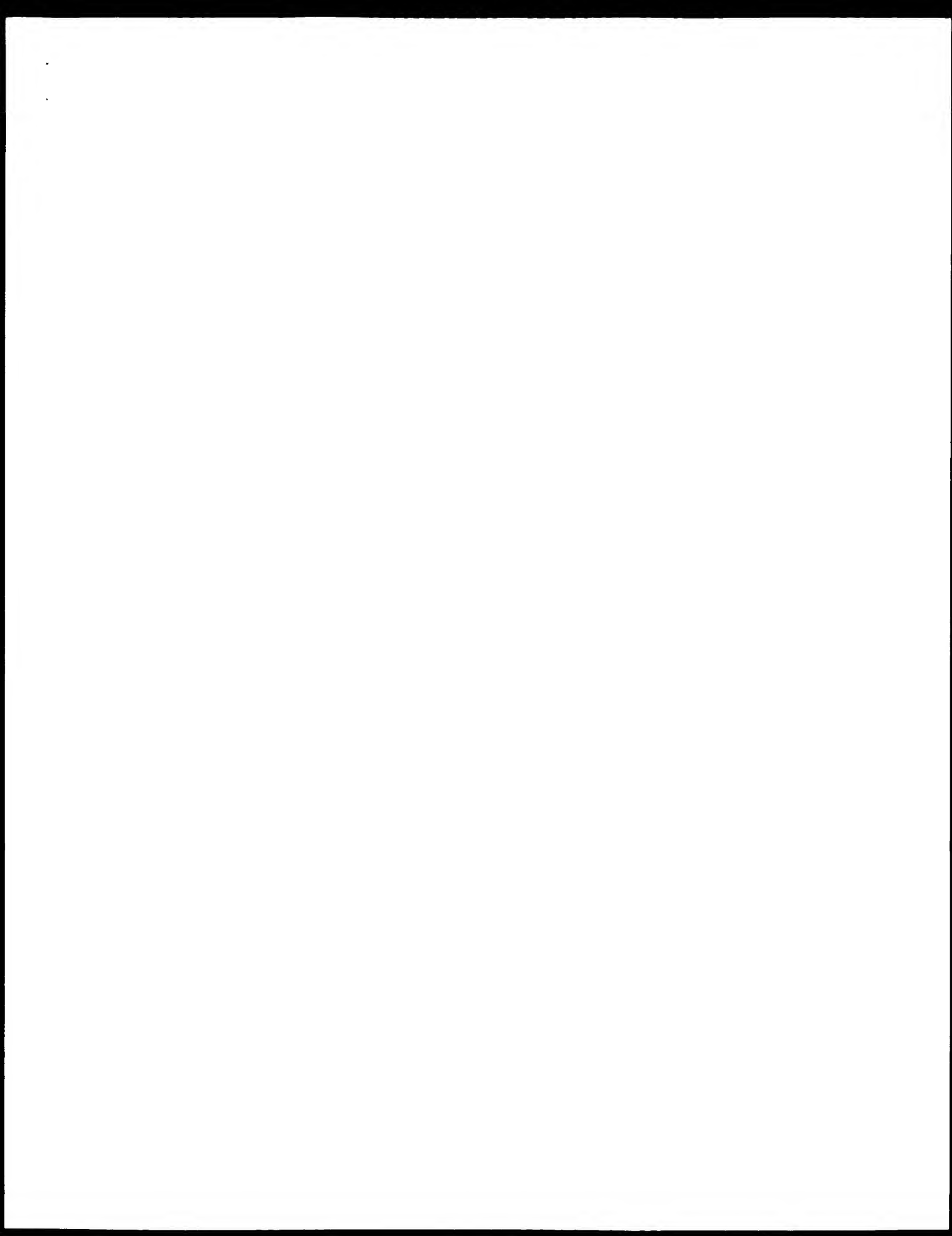
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Medicine, Division of Clinical Immunology, Karolinska Institute, P.O. Box 117, S-141 86 Huddinge, Sweden
Received by editor 1 October 1991
Accepted for publication 1 November 1991
(Pages 1 to 405)



CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense
 CC oligonucleotides). The proteins may be used to raise antibodies and to
 CC screen for modulators of activity, while the antibodies may be used to
 CC detect, and in drug targeting.

XX Sequence 610 BP; 155 A; 139 C; 114 G; 202 T; 0 other;

Query Match 100.0%; Score 402; Dp 21; Length 610;
 Best Local Similarity 100.0%; Pred. No. 1e-110;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 ACTTCCGATGTCACATGATGTTTATTACACCAAGAAACTGAGCAATGCTAGCA 60
 DB 181 ACTTCCGATGTCACATGATGTTTATTACACCAAGAAACTGAGCAATGCTAGCA 240
 UY 61 CTGTGACATGTCATCTTCTGCTGCAACCTTTTTCGCGCTATGCTCTCTT 120
 DB 241 CTGTGACATGTCATCTTCTGCTGCAACCTTTTTCGCGCTATGCTCTCTT 300
 UY 121 TATTAAAGCAAACTTTTGGAATAGTTTATCGACAGCAAGCTGCTGCTCTT 180
 DB 301 TATTAAAGCAAACTTTTGGAATAGTTTATCGACAGCAAGCTGCTGCTCTT 240
 UY 181 CAATGCTGTATACCTGCAAAACCTTTTAAATGACAGCTGCTGCTATTTTACG 240
 DB 361 CAATGCTGTATACCTGCAAAACCTTTTAAATGACAGCTGCTGCTATTTTACG 420
 UY 241 ACTAGCAATTCAGCTTCCATGCTATGACGCAAGTGGAGTGGACGACGCTCT 300
 DB 421 ACTAGCAATTCAGCTTCCATGCTATGACGCAAGTGGAGTGGACGACGCTCT 480
 UY 301 CAAGCTCTGTCACAGTCTATTCATGGAATTTCTACAGCAAGCAAGCAATAGG 360
 DB 481 CAAGCTCTGTCACAGTCTATTCATGGAATTTCTACAGCAAGCAAGCAATAGG 540
 UY 361 ACCGCAAGAGCTAGCAAACTCAAAATTCAGAGCAATTCGCT 402
 DB 541 ACCGCAAGAGCTAGCAAACTCAAAATTCAGAGCAATTCGCT 582

RESULT 5

AAE74300/c
 ID AAE74300 standard; DNA; 405 BP.

XX AAE74300;

XX 04-MAY-2001 (first entry)

XX Canine interleukin-5 coding sequence #1.

XX Dog; interleukin-5; IL-5; allergy; cancer; gene therapy;
 XX inflammatory reaction; ds.

XX Canis sp.

XX W020011049-A2.

XX 15-FEB-2001.

XX 09-AUG-2000; 2000W0-US21651.

XX 10-AUG-1999; 9908-0371615.

XX (HEX-) IDEXX LAB INC.

XX Guo H, Lawton R, Mermer H, Aiyappa AP;

DB W01-191942/19.
 DB P-PSB: AAE/2615.
 XX Novel canine interleukin-5 polynucleotide and polypeptides are used for
 PT generating antibodies which are useful in treating allergies in dogs -
 XX Claim 31; Page 46; 48pp; English.

XX The present invention provides the full length and coding sequences of the
 CC canine interleukin-5 (IL-5) protein. This can be used to treat allergies,
 CC cancer and inflammatory reactions in dogs. The present sequence is one
 CC version of the IL-5 coding sequence shown in the specification.

XX Sequence 405 BP; 131 A; 77 C; 94 G; 103 T; 0 other;

Query Match 99.2%; Score 298; Dp 22; Length 405;
 Best Local Similarity 99.5%; Pred. No. 8.1e-110;
 Matches 406; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

UY 1 ACTTCCGATGTCACATGATGTTTATTACACCAAGAAACTGAGCAATGCTAGCA 60
 DB 402 ACTTCCGATGTCACATGATGTTTATTACACCAAGAAACTGAGCAATGCTAGCA 343
 UY 61 CTGTGACATGTCATCTTCTGCTGCAACCTTTTTCGCGCTATGCTCTCTT 120
 DB 342 CTGTGACATGTCATCTTCTGCTGCAACCTTTTTCGCGCTATGCTCTCTT 283
 UY 121 TATTAAAGCAAACTTTTGGAATAGTTTATCGACAGCAAGCTGCTGCTCTT 180
 DB 282 TATTAAAGCAAACTTTTGGAATAGTTTATCGACAGCAAGCTGCTGCTCTT 223
 UY 181 CAATGCTGTATACCTGCAAAACCTTTTAAATGACAGCTGCTGCTATTTTACG 240
 DB 222 CAATGCTGTATACCTGCAAAACCTTTTAAATGACAGCTGCTGCTATTTTACG 303
 UY 241 ACTAGCAATTCAGCTTCCATGCTATGACGCAAGTGGAGTGGACGACGCTCT 300
 DB 362 ACTAGCAATTCAGCTTCCATGCTATGACGCAAGTGGAGTGGACGACGCTCT 363
 UY 301 CAAGCTCTGTCACAGTCTATTCATGGAATTTCTACAGCAAGCAAGCAATAGG 360
 DB 402 CAAGCTCTGTCACAGTCTATTCATGGAATTTCTACAGCAAGCAAGCAATAGG 423
 UY 361 ACCGCAAGAGCTAGCAAACTCAAAATTCAGAGCAATTCGCT 402
 DB 42 ACCGCAAGAGCTAGCAAACTCAAAATTCAGAGCAATTCGCT 461

RESULT 6

AA25550/c
 ID AA25550 standard; cDNA; 345 BP.

XX AA25550;

XX 14-MAR-2000 (first entry)

XX Canine mature interleukin-5 (IL-5) cDNA.

XX Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX Canis familiaris.

XX W09961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99W0-US11942.

XX 29-MAY-1998; 9808-0087306.

XX (HEX-) HESKA CORP.

111 cathepsins
 XX
 115 Discoloration, page 716; 134 fpp; 110 fpp
 XX
 116

The present invention describes a new composition comprising an active ingredient selected from (a) a compound having low adenosine triphosphatase activity, (b) a compound having low adenosine deaminase activity, or (c) a compound having both low adenosine triphosphatase and low adenosine deaminase activities, which has been found to be effective in the treatment of inflammation, asthma, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as lung cancer, lymphomas, sarcomas, and cancers which may metastasize to the lungs, including breast and prostate cancer. The production of the adenosine content of the compositions yields effects. The A-containing compounds break down with the release of deoxyadenosine which, in turn, promotes apoptosis resulting in bronchoconstriction and inflammation. AAAA2381 to AAAA612 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID Nos. 1 to 205, and then the last 185 sequences are also called SEQ ID No.1 to 185, but the sequences differ from the previously named sequences, SEQ ID No.1 to 185 (AAAA127 to AAAA912) are specifically claimed one from the present invention. N.P. sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID Nos. sequences given in the sequence listing.

NO	Sequences	Min BP	277 A	137 G	164 G	248 T	0 other
Dusty Match	69.0%	Score 277.2	4B 21	1604th 816			
Best Local Similarity	80.6%	Prod. No. 46674					
Matches 324	Conservation	0	Mismatches	78	Indels	0	Gaps
							0

07	1	AGCTTCAGGTCATACGCGCTGTTCATTCACGAGAAAGAAATCTGCGACGACGTCAGAA	60
08	445	AGCTTCATATATGCACTGCGCTTCATATACGAGAAAGAAATCTGCGACGACGTCAGAA	497
09	61	CTTCTGACGCTGCAATCTCTCTCTGCGAGACCTCTTTCTTCTGCGCGCTGACGCTCTCTT	120
10	186	TTCGCTTACCTCTGCGCTCTCTCTCTGCAACTCTTTCTTCTGCGCGCTGACGATCTCT	347
09	121	TATTAACACAACTCTTGAAATGCTTATGCAAGCACTGCTGCGCGCTGCGCGACCTTCTGCT	180
10	426	TATTAACAAAGATCTTTATATAGCTCTTCGCAATGACCTCTCTGCACTGCTATCTCT	247
09	181	TAATCTCTCTATATAGCTGAAAAAGCTCTTTAAAGCAAGCTCTGCACTTATTTATTTAGG	240
10	206	CAGCTGCTGCTATATGCTGAAATATCTCTGCACTGCGCACTTCTGATCTATAGG	267
09	211	AGTAAAGATCAATACGCTTCGCACTGCTATATCAAGCAAGCTCTGCACTGACGACGACTGT	300
10	206	AGCTTCATATATATACACTTCTGCACTGCTATATCAAGCAAGCTCTGCACTGACGACG	347
09	301	CAATCTCTCTGCTGCACTGCTATATCAAGCAAGCTCTGCACTGACGACGACGACGACG	360
10	146	CAATCTCTCTGCTGCACTGCTATATCAAGCAAGCTCTGCACTGACGACGACGACGACG	417
09	361	AGCTTCATATATATACACTTCTGCACTGCTATATCAAGCAAGCTCTGCACTGACGACG	427
10	86	AGCTTCATATATATACACTTCTGCACTGCTATATCAAGCAAGCTCTGCACTGACGACG	45

RESULT 15
AAE20980/7/
ID: AAE20980 standard: DNA: 4057 BP

AA	AA(2.7)801	1.4	MAH - 2001	(11751	e017y)
XX					
XX					

10E	Human 1w adenosine anti-sense oligonucleotide related sequence #2547.
XX	
KM	low adenosine anti-sense oligonucleotide; phosphorothioate; alveary;
KM	human airway disorder; bronchoconstriction; lung inflammation;
KM	anti-infective therapy; respiratory; bronchiolitis; and inflammation;
KM	immunorepressive; antiasthmatic; and/or hypoxemia; cytoskeletal
KM	cellulopathy; obstruction; pulmonary obstruction; improved respiratory
KM	anti-infective therapy; reduction; pulmonary vasoconstriction; asthma; RDS;
KM	respiratory distress syndrome; fatal; cystic fibrosis; allergic rhinitis;
KM	pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KM	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KM	cancer; SS.
XX	
XX	Human sapiens.
XX	
XX	W 2006/02716 A2.
XX	
XX	26 OCT 2000.
XX	
XX	24 MAR 2000; 2006W0 US080520.
XX	
XX	04 APR 1999; 1999S 0127958.
XX	
XX	(HHS) UNIV EAST CAROLINA.
XX	(HHS) NCI.
XX	
XX	NYCO JW.
XX	
XX	WFI; 2000 67957976.
XX	
XX	low adenosine (A) content anti-sense oligonucleotides which do not
XX	trigger adenosine receptors during metabolism, useful e.g. for treating
XX	cancers and respiratory obstructions.
XX	
XX	disclosure Page 788-789; 1594pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (1) comprising them. In the antisense oligonucleotides the A is replaced by a "universal" or alternative base. (1) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, anticholinergic, hypotensive and cytoskeletal activities. The antisense oligonucleotides and (1) can be used to down regulate the expression and/or activity of large polypeptides associated with lung/respiratory disorders and malfunctions, such as stimulant and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced serum and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non nervous system receptors, CNS and peripheral nervous and non nervous system peptide transmitters, detoxins, growth factors, vasoreactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (e.g., asthma), pulmonary obstruction and/or bronchoconstrictive disorder (e.g., bronchospasm, allergies), and/or pulmonary vasospasm, which are associated with a disease or condition selected from pulmonary vasospasm, inflammation, allergic asthma, emphysema, chronic obstructive pulmonary disease (COPD), hyperinflation, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, epinephrine, chronic obstructive pulmonary disease (COPD), pulmonary translation rejection, pulmonary infections, bronchitis, and/or cancer. AAT18134 to AAT21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.

Best Local Similarity 80.68; Pred. No. b. To 74;
Matches 324; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

```
|||||
100 4687 ACCTTATATAGCATGCGTGGTGTGATATACATCAAAAAAGCTCTGGACGTAAGCTGATACCA 3628
00 61 CTTCGACCTGCGATCTTCCTGCGACACCTTTTCTTGGCGCTCATGCTCTT 120
100 4627 TGGTTACGTCGCGCTTCTTGGCGACCTTTTCTTGGCGCATGATTTCT 3568
00 121 TATTAACAAATCTTTGSAATAGTTATGTCACAGCTGGCGGGGAGTTGGTCT 180
100 3567 TATTAAGGATCAATTTTGAATAGCTTTTGCACAGTACCTGCTGGACAGTTGACTCT 3508
00 181 CAATGCTCTATACCTTAAAAAGCTTTTAAAGCACTGGTGATTTTATTTTCTAG 240
100 3507 CATCTGCTCTATCTGCTGAAAGATTTCTTCACTGACACATGGTGATTTTATCTACAG 3448
00 241 ACTAGGAATCAAGATTCGCATGCGTATCTAGGCAATGCTATGAGTGGAGAGTCT 300
100 3447 AATAGGAATCTGATAGTCTCATAGCTATCTAGGCAAGTTGATGAGTGGAGAGTCT 3488
00 301 CAAGTCTCTGCAATCTATATATGGAATTTCTATATATTAAGGCAATATAGGC 360
100 3387 CAAGTCTCTCTTATATATATGCAATTTCTGGAATTTCTGGAATGGAATGCAATAGCTAGGC 3428
00 361 AATGCAAGCAATATATATATGCAATTTCTGGAATTTCTGGAATGGAATGCAATAGCTAGGC 402
100 3427 AATGCAAGCAATATATATATGCAATTTCTGGAATTTCTGGAATGGAATGCAATAGCTAGGC 3286
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Search completed: November 5, 2002, 11:17:41
Job time: 108.5 secs




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Db 321 ATTATGACAGATTTCGAAATATTCCTGATACAGCCGACCGACATTCGATCTTC 262
QY 182 AATGCTGCTAATGCTGAAAAATCTCTTTAATGACAGATCTGATTTTATTTACAGA 241
Db 261 AATATCTGATAGGCTGGAAGATTTTCCTAATGATAGCTGCTGATTTTATTCAGTACG 202
QY 242 GATGACATCATGCTGCTGCAATGCTATGATGATGATGATGATGATGATGATGATG 301
Db 201 ATGACAGAGCTGATGCTGATCTGCTGATGATGATGATGATGATGATGATGATGATG 142
QY 302 AATGCTGCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361
Db 141 AATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 95
QY 362 GATGACATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 421
Db 84 GATGACATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 50

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RESULT 4

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US-09-180-864-1/c
Sequence 1: Application US/0948064
Patent No. 645616

```

GENERAL INFORMATION:

```

APPLICANT: Lopez, Angel
APPLICANT: Vadas, Matthew
APPLICANT: Shannon, Frances
APPLICANT: Bastiras, Stan
APPLICANT: Hoy, Allan W
TITLE OF INVENTION: AN INTERFERIN 5 ANTAGONIST
FILE REFERENCE: 94722
CURRENT APPLICATION NUMBER: 08/299,799
CURRENT FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: 06/792,438
PRIOR FILING DATE: 1994-07-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 1
LENGTH: 477
TYPE: DNA
ORGANISM: nucleotide sequence encoding modified IL-5
FEATURE:
NAME/KEY: CDS
LOCATION: (4) -- (361)
US-09-180-864-1

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Query Match: 51.3% Score 206.2; DB 4; Length 377;
Best Local Similarity: 74.5% Freq. No. 120 56;
Matches 259; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

```

```

QY 12 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 71
Db 455 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 296
QY 72 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 131
Db 295 GATGACATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 236
QY 132 AATGCTGCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 191
Db 245 AATGCTGCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 176
QY 192 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 251
Db 175 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 116
QY 252 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
Db 115 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 56
QY 312 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 358
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RESULT 5

```

US-09-280-799-78/c
Sequence 78: Application US/0928079
Patent No. 6136603

```

GENERAL INFORMATION:

```

APPLICANT: Dean, Nicholas R
APPLICANT: Kufas, James R
APPLICANT: McKay, Robert
TITLE OF INVENTION: ANTIBODIES TO IL-5
FILE REFERENCE: 1538 6348
CURRENT APPLICATION NUMBER: 09/0728079
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 78
LENGTH: 420
TYPE: DNA
ORGANISM: Homo sapiens
US-09-280-799-78

```

```

Query Match: 24.7% Score 99.4; DB 4;
Best Local Similarity: 75.2% Freq. No. 4 60;
Matches 141; Conservative 0; Mismatches 11;

```

```

QY 238 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
Db 717 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
QY 311 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
Db 657 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
QY 358 GATGACATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
Db 597 GATGACATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311

```

RESULT 6

```

US-09-280-799-78/c
Patent No. 6136603

```

GENERAL INFORMATION:

```

APPLICANT: Honjo, Takaki; Honjo, Kiyoshige
TITLE OF INVENTION: HUMAN IL-5 RECEPTOR
PROTEIN OF PRODUCTION SALT FORM
NUMBER OF SEQ ID NOS: 2
CURRENT APPLICATION NO: 09/0728079
APPLICATION NUMBER: 09/0728079
FILING DATE: 21 SEP 1999
SEQ ID NO: 1
LENGTH: 420
US-09-280-799-78

```

```

Query Match: 24.7% Score 99.4; DB 4;
Best Local Similarity: 75.2% Freq. No. 4 60;
Matches 141; Conservative 0; Mismatches 11;

```

```

QY 238 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
Db 717 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
QY 311 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
Db 657 ATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
QY 358 GATGACATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
Db 597 GATGACATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311

```

RESULT 7

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US-08-629-640A-5/c

```

```

Sequence 5, Application: US/09/20643A
Patent No. 6025589
GENERAL INFORMATION:
APPLICANT: Lee, N. A.
TITLE OF INVENTION: IL-5 TRANSGENIC MOUSE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Schreiner, Lueders, Wessner & Kluth, P. A.
STREET: P. O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629,643A
FILING DATE:
CLASSIFICATION: B00
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/929,443
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viskochil, Ann S
REGISTRATION NUMBER: 37,748
REFERENCE/PATENT NUMBER: 150,167W01
INVENTOR INFORMATION:
TELEPHONE: 612-359,4260
TELEFAX: 612-359,4264
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6727 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: mat-peptide
LOCATION: 650..3771
OTHER INFORMATION: join 650..740, 1560..1592,
OTHER INFORMATION: 3468..3596, 3676..3771
US-08-629,643A 5
Query Match: 22.5% Score 90.6; EH 3; Length 6727;
Best Local Similarity: 76.6% Prog. No. 4,20-19;
Matches 11; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 83 CCGTAAACCTTTTGGGCGCTATGCTCTTTTATTAAGCAACGTTGGCAAT 142
DB 3610 CCGTAAACCTTTTGGGCGCTATGCTCTTTTATTAAGCAACGTTGGCAAT 3551
QY 143 AGTTATTCACAGCCCTCCCGGCGAGTTGATTTGCAATGCTGCAATACCTGAAA 202
DB 4550 AGCATTTCCACAGTACCGGCGAGTTGATTTGCAATGCTGCAATACCTGAAAAG 3491
QY 203 ACTTTTAAATGCAATTTGGTAT 227
DB 4490 ATTTCGAAATGCAATTTGGTAT 4466

```

```

TITLE OF INVENTION: ANTISENSE MIMOTIC RIBONUCLEOTIDE SIGNAL
FILE REFERENCE: ISM 0340
CURRENT APPLICATION NUMBER: US/09/280,799
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Paton In Ver. 2.0
SEQ ID NO: 1
LENGTH: 6727
TYPE: DNA
ORGANISM: Mus musculus
US-09-280-799-1
Query Match: 22.5% Score 90.6; EH 3; Length 6727;
Best Local Similarity: 76.6% Prog. No. 4,20-19;
Matches 11; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 83 CCGTAAACCTTTTGGGCGCTATGCTCTTTTATTAAGCAACGTTGGCAAT 142
DB 3610 CCGTAAACCTTTTGGGCGCTATGCTCTTTTATTAAGCAACGTTGGCAAT 3551
QY 143 AGTTATTCACAGCCCTCCCGGCGAGTTGATTTGCAATGCTGCAATACCTGAAA 202
DB 4550 AGCATTTCCACAGTACCGGCGAGTTGATTTGCAATGCTGCAATACCTGAAAAG 3491
QY 203 ACTTTTAAATGCAATTTGGTAT 227
DB 4490 ATTTCGAAATGCAATTTGGTAT 4466

```

```

RESULT 5
US-09-155-834-5/6
Sequence 5, Application: US/09/159884
Patent No. 6215040
GENERAL INFORMATION:
APPLICANT: James J. Lee et al.
TITLE OF INVENTION: IL-5 TRANSGENIC MOUSE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: Schreiner, Lueders, Wessner & Kluth, P. A.
STREET: P. O. Box 2938
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/155,884
FILING DATE: Unknown
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/05932
FILING DATE: 09-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Viskochil, Ann S
REGISTRATION NUMBER: 37,748
REFERENCE/PATENT NUMBER: 150,167W02
INVENTOR INFORMATION:
TELEPHONE: 612-359-3260
TELEFAX: 612-359-3061
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6727 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
FEATURE:

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Sequence 244, Application US/0945702B
Patent No. 6365724

GENERAL INFORMATION:
APPLICANT: Blument, Frederick R.
Barland, Valerie
Penna, Nicole T.
Flunkert, Guy
Wolch, Rod

TITLE OF INVENTION: No. 6365724: Sequences of E. coli G157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles A Brady
STREET: 1 South Pinekey Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0945702B
FILING DATE: 04 Dec-1999
CLASSIFICATION: unknown

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 68/110,955
FILING DATE: 04 Dec-1998

AUTHOREY/ACRDI INFORMATION:
NAME: Spay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/SEQUENCE NUMBER: 960296,95017

TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166

INFORMATION FOR SEQ ID NO: 244:
SEQUENCE CHARACTERISTICS:
LENGTH: 2797
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 244:
US 09-45702B-244

[illegible]

Search completed: November 7, 2002, 21:36:41
Job time : 36.1333 secs



Genome version 5.1.3
Copyright (c) 1993 - 2002 Computer Ltd.

OM nucleic - nucleic search, using SW model

Run on: November 7, 2002, 08:51:15 : Search time 745 Seconds

(without alignment)
8739.041 Million cell updates/sec

Title: us-09-755-633-8

Percent score: 402
Sequence: 1 acattccagatgacatcgag.....aatccagatgacatcgat 402

Scoring table:
Gapop 10.0 / Gapext 1.0

Searched: 16154066 seqs, 8077743376 residues

Total number of hits satisfying chosen parameters: 42308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 08

Maximum Match: 1008
Listing first 45 summaries

Database:

ES1:
1: em_estbna:
2: em_estbna:
3: em_estbna:
4: em_estbna:
5: em_estbna:
6: em_estbna:
7: em_estbna:
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	19.4	503	14	B0598873 MI-P-E4-a
2	40.6	10.1	522	13	B1670794 P1EST0a0
3	39.8	9.9	535	17	AZ370501 IM0121K03
4	39.2	9.8	603	13	B1328562 B1328562
5	39.2	9.8	619	13	B1328562 B1328562
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18	36.8	9.2	153	1	B1328562
19	36.6	9.1	153	1	B1328562
20	36.4	9.1	153	1	B1328562
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22	36.4	9.1	153	1	B1328562
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44	35.6	8.9	153	1	B1328562
45	35.6	8.9	153	1	B1328562

REFERENCES

RESULT 1
B0598873
DEFINITION
MI-P-E4-a
ACCESSION
B0598873
VERSION
B0598873.1
KEYWORDS
EST,
SOURCE
SUS SCROFA
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

Molecular Genetics Laboratory, Department
Iowa State University
201 Kildee Hall, Ames, IA 50011-0100, USA
Tel: 515/294-4400
Fax: 515/294-4400
Email: ckuang@iastate.edu
Tissue procurement: Dr. Chris Jorgensen, Iowa
CIRIA Library, Department of Molecular Biology,
Iowa State University, Ames, IA 50011-0100, USA
DNA Sequencing: Dr. Chris Jorgensen, Iowa State University

BASE COUNT 280 a 148 c 171 g 239 t
 ORIGIN KKGCEWPKKKHLYLQVLEVINIEMIMES"

Query Match 8.7% Score 30; DB 4; Length 838;
 Best Local Similarity 100.0%; Prod. No. 4.1e-05;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 AACTTGTCTTAATAAAGACACATAGA 239
 DB 311 AACTTGTCTTAATAAAGACACATAGA 340

RESULT 15
 AF294756 405 bp mRNA 1150bp FRI 10 MAY 2002
 LOCUS Saimiri sciureus Interleukin-5 mRNA, complete cds.
 ACCESSION AF294756
 VERSION AF294756.1 GI:15213529
 KEYWORDS
 SOURCE Saimiri sciureus.
 ORGANISM Saimiri sciureus.
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae;
 Saimiri.

REFERENCE 1 (bases 1 to 405)
 AUTHORS Herard J.M., Lavergne A. and Kazanji M.
 TITLE Molecular cloning, characterization, and quantification of squirrel monkey (Saimiri sciureus) Th1 and Th2 cytokines

JOURNAL Immunogenetics 54 (1), 20-29 (2002)
 MEDLINE 21972723
 PubMed 11976788

REFERENCE 2 (bases 1 to 405)
 AUTHORS Herard J.M., Lavergne A. and Kazanji M.
 TITLE Direct Submission
 JOURNAL Submitted (09-AUG-2000) Pasteur Institute, Institut Pasteur de la Guyane, 27, Avenue Pasteur, Cayenne 97306, French Guiana

FEATURES
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 /protein_id="AAK9204.1"
 /db_xref="GI:15213530"
 /translation="MPMLHLISLALGAHWCAHPAPPSAI VETLAI DSTRPTL
 MVRTELLEVAHNEICCTPTFGCTGT ENCTVCGSVFKI PONTSLIKHIDRQK
 KKGCEWPKKKHLYLQVLEVINIEMIMES"

BASE COUNT 129 a 84 c 95 g 97 t
 ORIGIN

Query Match 8.1% Score 28; DB 9; Length 405;
 Best Local Similarity 100.0%; Prod. No. 0.00052;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 307 TTCTTGTTGTAATAACACCATGGA 334
 DB 364 TTCTTGTTGTAATAACACCATGGA 391

Search completed: November 7, 2002, 21:40:51
 Job time: 981.587 secs



Fri Nov 8 12:51:46 2002

us-09-755-633-9.rst

Page 8

Job time : 640.547 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2002, 08:51:15 : Search time 078.644 Seconds

(without alignments) 10259.568 Million cell updates/sec

Title: US-09-755-633-9

Perfect score: 345

Sequence: 1 ttgctgtgtaaaataacacat.....ccgattgacacacacaaat 345

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl : *

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2: gb_ba : *

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4: gb_ba : *

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6: gb_ba : *

7: gb_ba : *

8: gb_ba : *

9: gb_ba : *

10: gb_ba : *

11: gb_ba : *

12: gb_ba : *

13: gb_ba : *

14: gb_ba : *

15: gb_ba : *

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41: gb_ba : *

score greater than or equal to the score of the first
and is derived by adding 5 to the total score of the

SUMMARIES

Result No.	Score	Query Match	Length (bp)	
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5	289.6	83.9	418	AF092436
6	285.4	82.7	405	AF088770
7	283.8	82.3	405	AF081105
8	280	81.2	429	SS0134452
9	278.4	80.7	405	SS010058
10	274.8	79.7	420	AF081038
11	273.4	79.2	424	AF081372
12	250	72.5	41	AX080948
13	234.6	68.0	405	AF234756
14	231.4	67.1	406	AF08155A
15	231.4	67.1	415	AF081439
16	231.4	67.1	415	AF081439
17	231.4	67.1	415	AF081439
18	229.8	66.6	417	AF081439
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20	224.6	65.1	417	AF081439
21	224.6	65.1	417	AF081439
22	206.6	59.9	417	AF081439
23	206	59.7	417	AF081439
24	205	59.7	417	AF081439
25	196.4	56.9	417	AF081439
26	196.4	56.9	417	AF081439
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34	191.6	55.5	417	AF081439
35	190.6	55.2	417	AF081439
36	190	55.1	417	AF081439
37	189	54.8	417	AF081439
38	178.4	51.7	417	AF081439
39	175.6	50.9	417	AF081439
40	169.2	49.0	417	AF081439
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42	166	48.1	417	AF081439
43	165.6	48.0	417	AF081439
44	161.6	46.8	417	AF081439
45	160.4	46.5	417	AF081439

ALIGNMENTS

RESULT 1

AF331919

LOCUS AF331919

DEFINITION Canis familiaris Interleukin-5 mRNA, complete

ACCESSION AF331919

VERSION AF331919.1 GI:1041090

KEYWORDS

SOURCE

ORGANISM

Canis familiaris

Eukaryote; Mammalia; Canidae; Canis

1 (bases 1 to 410)

Yand.S., Solinas-Krus, Weber, E., and McNeil

Canine Interleukin-5: Molecular Characterization

expression of biologically active recombinant

Prod. No. is the number of results predicted by chance to have a

REFERENCES
 BERNARD, H. 1969. *Opisthotropus*, *Peromyscus*, *Neotoma*, *Neotomastoma*, *Mammalia*: Insectivora, Primates, Carnivores, Peromyscoidae, Peropithecoidae, Peropithecines, Cercopithecoidea, 1 (bases 1 to 405).

XX claim the Page 226-227: 264pp: English.
 JS
 XX
 CC Sequences AA25546 represent cDNA sequences encoding
 CC canine Interleukin-5 (IL-5). The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony stimulating factor (GM-CSF), and nucleotide sequences which
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleotide acids, specific antibodies and inhibitors may be used as
 CC vaccines for the therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumors, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense
 CC oligonucleotides). The proteins may be used to raise antibodies and to
 CC screen for modulators of activity, while the antibodies may be used in
 CC detection, and in drug targeting.

XX
 SU Sequence 445 bp: 120 A: 68 G: 78 C: 79 T: 0 other:
 Query Match: 100.0%; Score 445; 18 21; Length 345;
 Best local similarity: 100.0%; Prot. No. 2,26-94;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 TTGCTGTGTAATAATGATGAATACCTGGGCGAGAACTTACATCTGCTGCACCT 60
 YY 61 CATGCAACTTGGCTGTAATGCGATGGAACCTGATCTGCTGCTGCTGAAATAAATA 120
 |||||||
 DB 61 CATGCAACTTGGCTGTAATGCGATGGAACCTGATCTGCTGCTGCTGAAATAAATA 120
 YY 121 CAGCAATGCTGATTAATAAAGATTTTAAAGTATAGAAATATTAAGAAATGCT 180
 |||||||
 DB 121 CAGCAATGCTGATTAATAAAGATTTTAAAGTATAGAAATATTAAGAAATGCT 180
 YY 181 CAGCGGAAAGCTGTGATTAATATATCTCAAACTGCTCTTAATTAATAAATAATATAG 240
 |||||||
 DB 181 CAGCGGAAAGCTGTGATTAATATATCTCAAACTGCTCTTAATTAATAAATAATATAG 240
 YY 241 CAGCAATGCTGATTAATAAAGATTTTAAAGTATAGAAATATTAAGAAATGCT 300
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 DB 241 CAGCAATGCTGATTAATAAAGATTTTAAAGTATAGAAATATTAAGAAATGCT 300
 YY 401 CAGGTAATTTTGCTGTGTAATAAAGCTGAGTGGACAGCTGAAACT 445
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 DB 401 CAGGTAATTTTGCTGTGTAATAAAGCTGAGTGGACAGCTGAAACT 445

RESULT 2

AA25551/:

ID AA25551 standard: cDNA: 345 bp.

AC AA25551:

DI 14-MAR-2000 (first entry)

DE Canine mature Interleukin 5 (IL-5) cDNA complement.

XX Interleukin 5 (IL-5) antibody; Canine; Inhibitor; Immune response;

XX Immunoregulation; Tumour; Cancer; Autoimmune disease; Vaccine; SS.

XX Canis familiaris.

OS Canis familiaris.

XX W09961618-A2

XX 02-DEC-1999.

XX

PE 29 MAY-1999: 9980-US11942.
 XX
 PR 29 MAY-1998: 98US-0087406.
 XX
 PA (HEK3) HESKA (OKR) .
 XX
 PI Shim G., Yama S., Freilitz M., Wondolilind RS:
 XX
 XX W011, 2000 07262706.
 DB P-PSH8: AA2555220.

XX
 CC Claim the Page 226: 264pp: English.
 JS
 XX
 CC Sequences AA25546 25551 represent cDNA sequences encoding
 CC canine Interleukin-5 (IL-5). The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotide sequences which
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleotide acids, specific antibodies and inhibitors may be used as
 CC vaccines for the therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumors, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense
 CC oligonucleotides). The proteins may be used to raise antibodies and to
 CC screen for modulators of activity, while the antibodies may be used in
 CC detection, and in drug targeting.

XX
 SU Sequence 345 bp: 79 A: 78 G: 68 C: 120 T: 0 other:
 Query Match: 100.0%; Score 445; 18 21; Length 445;
 Best local similarity: 100.0%; Prot. No. 2,26-94;
 Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 1 TTGCTGTGTAATAATGCCATTAATATATCTGGTGAAGAACTTGAATCTGCTGCACCT 60
 |||||||
 DB 445 TTGCTGTGTAATAATGCCATTAATATATCTGGTGAAGAACTTGAATCTGCTGCACCT 60
 YY 61 CATGCAACTTGGCTGTAATGCGATGGAACCTGATCTGCTGCTGCTGAAATAAATA 120
 |||||||
 DB 285 CATGCAACTTGGCTGTAATGCGATGGAACCTGATCTGCTGCTGCTGAAATAAATA 120
 YY 121 CAGCAATGCTGATTAATAAAGATTTTAAAGTATAGAAATATTAAGAAATGCT 180
 |||||||
 DB 225 CAGCAATGCTGATTAATAAAGATTTTAAAGTATAGAAATATTAAGAAATGCT 180
 YY 181 CAGCGGAAAGCTGTGATTAATATATCTCAAACTGCTCTTAATTAATAAATAATATAG 240
 |||||||
 DB 185 CAGCGGAAAGCTGTGATTAATATATCTCAAACTGCTCTTAATTAATAAATAATATAG 240
 YY 241 CAGCAATGCTGATTAATAAAGATTTTAAAGTATAGAAATATTAAGAAATGCT 300
 |||||||
 DB 105 CAGCAATGCTGATTAATAAAGATTTTAAAGTATAGAAATATTAAGAAATGCT 300
 YY 401 CAGGTAATTTTGCTGTGTAATAAAGCTGAGTGGACAGCTGAAACT 445
 |||||||
 DB 45 CAGGTAATTTTGCTGTGTAATAAAGCTGAGTGGACAGCTGAAACT 1

RESULT 3

AA25548

ID AA25548 standard: cDNA: 402 bp.

AC AA25548:

XX

Sequence 1: Application 05/0918064
 Patient No. 6465616
 GENERAL INFORMATION:
 APPLICANT: H. F. J. D. P.
 APPLICANT: Adams, Matthew
 APPLICANT: Shannon, Frances
 APPLICANT: Hostiles, Stan
 APPLICANT: Hoy, Allison
 TITLE OF INVENTION: AN INTERLOCKING 5-ARMAMENT
 FILE REFERENCE: 927-28
 CURRENT APPLICATION NUMBER: 99-07-064
 CURRENT FILING DATE: 1999-04-12
 PRIOR APPLICATION NUMBER: 69-791,438
 PRIOR FILING DATE: 1994-07-28
 NUMBER OF SEQ TO NEST: 2
 SOFTWARE: Patented Vol. 2.1
 SEQ. ID No. 1
 LENGTH: 477
 TYPE: DNA
 ORGANISM: nucleotide sequence encoding modified 11-5
 FEATURE:
 NAME/KEY: C3G
 LOCATION: (4)...(466)
 75-019-180-864 1

Query Match	59.7%	Score	254	Exp. 1	Identical	37%	
Best Local Similarity	77.0%	Prod. No.	2,56-56				
Matches 251	0	Mismatches	75	Indels	0	Gaps	0

[illegible]

RESOLUTION 3
US-08-629-643A 4
Sequence 4, Applicant from US/08-29643A
Patent No. 6025539
GENERAL INFORMATION:
APPLICANT: Lee, J. L.
APPLICANT: Lee, N. A.
TITLE OF INVENTION: 11-5 TRANSDUCING MOUTH
NUMBER OF SEQUENCES: 5
CORRESPONDENT ADDRESS:
ADDRESS: Schwabach, Lindert, Weiss
STREET: P. O. Box 2948
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible

1 OPERATING SYSTEM: DOS
2 SOFTWARE: FAST-SEO Version 2.0
3 CURRENT APPLICATION DATA:
4 ALERT ACTION NUMBER: 0020203641A
5 FILING DATE:
6 CLASSIFICATION: 800
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: 09/429,643
9 FILING DATE: 09-APR-1996
10 ATTORNEY/AGENT INFORMATION:
11 NAME: VERSHUIS, Ann S
12 REGISTRATION NUMBER: 72,742
13 REFERENCE/TWENTY NUMBER: 160,167001
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 612-459-3240
16 TELEFAX: 612-459-3263
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[illegible]

1 RESULT 4
 2 US-09-15-884-4
 3 Sequence 4, Application US/09155884
 4 Patent No. 6215040
 5 GENERAL INFORMATION:
 6 APPLICANT: James J. Lee et al.
 7 TITLE OF INVENTION: IL-5 INHIBITING MOIST
 8 NUMBER OF SEQUENCES: 5
 9 CORRESPONDENCE ADDRESS:
 10 ADDRESSEE: Schwabman, Lundberg, Woessner & Kluth, P. A.
 11 STREET: P. O. Box 2938
 12 CITY: Minneapolis
 13 STATE: MN
 14 COUNTRY: USA

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1 ZIP: 55402
2 COMPUTER READABLE FORM:
3 MEDIUM TYPE: Diskette
4 COMPUTER: IBM Compatible
5 OPERATING SYSTEM: DOS
6 SOFTWARE: FASTSEQ Version 2.0
7 CURRENT APPLICATION DATA:
8 APPLICATION NUMBER: US/09/755,984
9 FILING DATE: Unknown
10 CLASSIFICATION:
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: 09/067,096
13 FILING DATE: 09-APR-1997
14 ATTORNEY/AGENT INFORMATION:
15 NAME: VIKSINS, Ann S
16 REGISTRATION NUMBER: 47,748
17 REFERENCE/SEQUENCE NUMBER: 150,167,182
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: 612-359-4260
20 TELEFAX: 612-359-4061
21 TELEX:
22 INFORMATION FOR SEQ ID NO: 4:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 1544 base pairs
25 TYPE: nucleic acid
26 STRANDEDNESS: Single
27 MOLECULE TYPE: cDNA
28 FEATURE:
29 NAME/KEY: mat.ppt.110
30 LOCATION: 104...442
31 OTHER INFORMATION:
32 US-09-155-884-4
33
34 Query Match: 54.9% Score 196.4 E-4 Length 1544
35 Best Local Similarity: 73.4% Pred. No. 5,56-53
36 Matches: 251, Conserved: 93, Mismatches: 21, Indels: 0, Gaps: 6,
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DB 1881 AGATGATTTTGTACTGACAAAGTCTTGAAGGAAAGACACAGTGCAGAGTCAAGCTG 1940
 GY 179 CCCAGCGGAGGCTGTGGATTAACATATTCGAAAGCTGCTTATTAAGAACACATAG 238
 DB 1941 TCGAAGCGGCTGCTGTGGAAAGACTATTCAAAAGCTGTCTTATTAAGAAATACATG 2000
 GY 239 AAGCGCAAAAAAAGAGTGTGA 261
 DB 2001 AAGCGCAAAAAAAGTACACCA 2023

RESULT 10

US-08-232-463-14/C
 Sequence 14, Application US/08232463
 Patent No. 5670367
 GENERAL INFORMATION:
 APPLICANT: DORNER, F.
 APPLICANT: SCHUELLINGER, F.
 APPLICANT: FALKNER, F.G.
 TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22313-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,463
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/997,313
 FILING DATE:
 APPLICATION NUMBER: EP 91 114 300.6
 FILING DATE: 26-08-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,769
 REFERENCE/DOCKET NUMBER: 20422,111; 1887
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)836-9300
 TELEFAX: (703)683-4109
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7218 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 CLONE: pTZapl-F15
 US-08-232-463-14

Query Match 11.0%; Score 38; DB 1; Length 7218;
 Best Local Similarity 9.5%; Prod. NO. 0.024;
 Matches 70; Consistency 14%; Mismatches 131; Indels 0; Gaps 0;

DB 1500 GAGCTTACAGCTGCTGCACATCAAGCACTTGGCTGATAGAGTATGAGAA GTGAGCA 98
 GY 49 GAGCTTACAGCTGCTGCACATCAAGCACTTGGCTGATAGAGTATGAGAA GTGAGCA 98
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 GY 99 TCGTACTGCTAAATAAATAATACGACAGCTGCTGATTAAGCACTTTTCAAGTATAGA 158
 DB 1440 TCGTACGPP 1381
 GY 159 CACATTAATTAAGCAAAATATCTGATGCTGATTAATTAATTAATTAATTAATTAATTA 219

DB 1380 PPP 1380
 GY 219 TTTAATAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1380
 DB 1320 PPP 1320
 GY 279 CACAAAGTGTCTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1320
 DB 1260 PPP 1260
 GY 339 GGAAG 344
 DB 1200 RRRRR 1195

RESULT 11

US-08-986-485-1/C
 Sequence 1, Application US/08986485
 Patent No. 6046030
 GENERAL INFORMATION:
 APPLICANT: WU, SHULIAN
 APPLICANT: SWEET, KAYMAN
 APPLICANT: TRENCH, ALFRED
 TITLE OF INVENTION: A HUMAN L10-1 HOMOLOG (H-10-1)
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WATNER & PIERCE
 STREET: P.O. Box 900
 CITY: VALLEY Forge
 STATE: PA
 COUNTRY: USA
 ZIP: 19482
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/986,485
 FILING DATE: 08-09-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/460,448
 FILING DATE: 22-Sep-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: PRESTIA, PAUL F.
 REGISTRATION NUMBER: 24,054
 REFERENCE/DOCKET NUMBER: 08 7 264
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0700
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4843 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-986-485-1

Query Match 10.0%; Score 34.4; DB 1;
 Best Local Similarity 6.8%; Prod. NO. 0.28;
 Matches 71; Consistency 10%; Mismatches 61;

DB 106 CTGCAAAATTAATAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 106
 GY 3659 CTGCAATACGAAAAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTA 106
 DB 106 AATCAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 106
 GY 3659 AATCAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 106




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? FILING DATE: 22 MAR 1996
? CLASSIFICATION: 514
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: GB 9505784.0
? FILING DATE: 22-MAR-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: Drogot, Walter H.
? REGISTRATION NUMBER: 21,196
? REFERENCE/DOCUMENT NUMBER: A-63316
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 781-1989
? TELEFAX: (415) 398-3249
? INFORMATION FOR SEQ ID NO: 48:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 21 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? HYPOHEMICAL: NO
? ANTI-SENSE: NO
US-08-621-841-48

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Query Match 5.28; Score 18; DB 3; Length 21;
Best Local Similarity 100.0%; Prod. No. 8.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 113 ATAAATGACCACTG 130
DB 4 ATAAATGACCACTG 21

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RESULT 7
US-09-328-111-666
? Sequence 666, Application 03/03/2011
? Patent No. 622333
? GENERAL INFORMATION:
? APPLICANT: Endege, Wilson O.
? APPLICANT: Steinmann, Kathleen E.
? APPLICANT: Astle, Jon H.
? APPLICANT: Burgess, Christopher C.
? APPLICANT: Bushnell, Steven E.
? APPLICANT: Carroll III, Eddie
? APPLICANT: Catino, Theodore J.
? APPLICANT: Dertli, Adrian
? APPLICANT: Ford, Donna M.
? APPLICANT: Lewis, Marcia E.
? APPLICANT: Monahan, John E.
? APPLICANT: Schlegel, Robert
? TITLE OF INVENTION: N-VEL. HUMAN GINES AND GENE EXPRESSION
? TITLE OF INVENTION: PRODUCTS
? FILE REFERENCE: CDD-257 (US)
? CURRENT APPLICATION NUMBER: US/06/028,111
? CURRENT FILING DATE: 1999-06-08
? EARLIER APPLICATION NUMBER: US 60/588,201
? EARLIER FILING DATE: 1998-05-10
? NUMBER OF SEQ ID NOS: 850
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 666
? LENGTH: 349
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-328-111-666

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Query Match 4.99; Score 17; DB 1; Length 312;
Best Local Similarity 100.0%; Prod. No. 25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 188 AAGCTGCGAATACTA 204
DB 192 AAGCTGCGAATACTA 208

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RESULT 8

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US-09-280-116-171
? Sequence 171, Application 03/03/2001.5A
? Patent No. 6331427
? GENERAL INFORMATION:
? APPLICANT: Robinson, Keith E.
? TITLE OF INVENTION: Nucleic Acid Molecules Encoded by
? FILE REFERENCE: 5800 24, 05/00/176/965
? CURRENT APPLICATION NUMBER: US/06/280,116A
? CURRENT FILING DATE: 1999-05-26
? NUMBER OF SEQ ID NOS: 268
? SOFTWARE: PatentIn Ver 7.0
? SEQ ID NO 171
? LENGTH: 823
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: protein-coding regions
US-09-280-116-171

```

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Query Match 4.99; Score 17; DB 1; Length 312;
Best Local Similarity 100.0%; Prod. No. 24;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 101 CTACTCTGAAAAAATA 113
DB 681 CTACTCTGAAAAAATA 99

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RESULT 9
US-08-869-137-170
? Sequence 1, Application 03/03/2001.5A
? Patent No. 5856157
? GENERAL INFORMATION:
? APPLICANT: Salzman, David
? APPLICANT: Gray, Richard
? APPLICANT: Medford, David
? APPLICANT: Mamm, Ron
? APPLICANT: Fox-Roston, Daniel
? TITLE OF INVENTION: A No. 08/06,3701 09 14:00:00
? TITLE OF INVENTION: A No. 08/06,3701 09 14:00:00
? NUMBER OF SEQUENCES: 2
? CORRESPONDENCE ADDRESS:
? ADDRESS: The West Law Firm
? STREET: 700 Koppers Blvd.
? CITY: Pittsburgh
? STATE: PA
? COUNTRY: USA
? ZIP: 15219-1818
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq for Windows Version 2.0
? CURRENT APPLICATION NUMBER: US/06/028,111
? CURRENT FILING DATE: 1999-06-08
? EARLIER APPLICATION NUMBER: US 60/588,201
? EARLIER FILING DATE: 1998-05-10
? NUMBER OF SEQ ID NOS: 850
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 666
? LENGTH: 349
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: protein-coding regions
US-09-280-116-171

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100%: linear
 NAME: 17
 LOCATION: 17
 OTHER INFORMATION:

US-09-455-702B-96
 Query Match: 4.9%, Score 17, DB 4, Length 1537
 Best Local Similarity: 100.0%, Pred. No. 24
 Matches: 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0

170 ACCTGAAAAATGAC 186
 DB 431 ACCTGAAAAATGAC 415

RESULT 10
 US-09-418-448-42
 Sequence 12, Application US/09418448
 Patent No. 6,210,950
 GENERAL INFORMATION:
 APPLICANT: Johnson, William G.
 APPLICANT: Stevens, Edward S.
 TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
 FILE REFERENCE: 601-1-057
 CURRENT APPLICATION NUMBER: 09/09418448
 CURRENT FILING DATE: 1999-05-25
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: Patonlin Ver. 2.0
 SEQ ID NO: 42
 LENGTH: 1547
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-418-448-42

Query Match: 4.9%, Score 17, DB 4, Length 1537
 Best Local Similarity: 100.0%, Pred. No. 24
 Matches: 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0

US-09-455-702B-96
 Query Match: 4.9%, Score 17, DB 4, Length 1537
 Best Local Similarity: 100.0%, Pred. No. 24
 Matches: 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0

NAME: Dan, William T
 REGISTRATION NUMBER: 34,344
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 608-270-5219
 TELEFAX: 610-270-5090

US-09-455-702B-96
 Query Match: 4.9%, Score 17, DB 4, Length 1537
 Best Local Similarity: 100.0%, Pred. No. 24
 Matches: 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0

107 CCGAAAAATGAC 124
 DB 1203 CCGAAAAATGAC 1219

RESULT 12
 US-09-455-702B-96
 Sequence 12, Application US/09455702B
 Patent No. 6,657,243
 GENERAL INFORMATION:
 APPLICANT: Battner, Frederick R.
 APPLICANT: Penn, Nicole F.
 APPLICANT: Plunkett, Guy
 APPLICANT: Wolf, Rod
 TITLE OF INVENTION: NOVEL SEQUENCES OF EXON 1
 FILE REFERENCE: 601-1-057
 CURRENT APPLICATION NUMBER: 09/09455702B
 CURRENT FILING DATE: 1999-05-25
 NUMBER OF SEQ ID NOS: 265
 SOFTWARE: Word Perfect 8.0
 SEQ ID NO: 1
 LENGTH: 1547
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-455-702B-96

Query Match: 4.9%, Score 17, DB 4, Length 1537
 Best Local Similarity: 100.0%, Pred. No. 24
 Matches: 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0

US-09-455-702B-96
 Query Match: 4.9%, Score 17, DB 4, Length 1537
 Best Local Similarity: 100.0%, Pred. No. 24
 Matches: 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0

Best Local Similarity: 100.0%; Pred. No. 21;
Matches: 17; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0.

QY 113 ATAAATCACCACG 129
|||||

Db 32233 ATAAATCACCACG 22479

RESULT 13

US-08-375-709-1

Sequence 1, Application US/08375709

Patent No. 5681898

GENERAL INFORMATION:

APPLICANT: YAZAWA, Kazuhiro

APPLICANT: YAMADA, Akiko

APPLICANT: KATO, Seishi

APPLICANT: KONDO, Kiyoshi

TITLE OF INVENTION: Gene Coding for Elcosapentaenoic Acid

TITLE OF INVENTION: Synthesizing Enzymes and Process for Production of

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESS: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08375709

FILING DATE: 20-JAN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/178,251

FILING DATE: 14-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-147945

FILING DATE: 15-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: WESSNER, Harold G.

REGISTERED ADDRESS: 25,258

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 37895 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: *Shewanella putrefaciens* SCKC 2874 (FERM

US-08-375-709-1

Query Match: 4.9%; Score 17; DB 1; Length 37895;

Best Local Similarity: 100.0%; Pred. No. 21;

Matches: 17; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 315 TGIATAAACACCGAGT 331
|||||

Db 1195 TGIATAAACACCGAGT 1211

RESULT 14

US-08-753-929-1
Sequence 1, Application US/08753929
Patent No. 5798259

GENERAL INFORMATION:

APPLICANT: YAZAWA, Kazuhiro

APPLICANT: YAMADA, Akiko

APPLICANT: KATO, Seishi

APPLICANT: KONDO, Kiyoshi

TITLE OF INVENTION: Gene Coding for Elcosapentaenoic Acid

TITLE OF INVENTION: Synthesizing Enzymes and Process for Production of

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESS: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08753929

FILING DATE: 20-JAN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/178,251

FILING DATE: 14-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4-147945

FILING DATE: 15-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: WESSNER, Harold G.

REGISTERED ADDRESS: 25,258

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 37895 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: *Shewanella putrefaciens* SCKC 2874 (FERM

US-08-753-929-1

Query Match: 4.9%; Score 17; DB 1; Length 37895;

Best Local Similarity: 100.0%; Pred. No. 21;

Matches: 17; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 315 TGIATAAACACCGAGT 331
|||||

Db 1195 TGIATAAACACCGAGT 1211

RESULT 15

US-09-090-793-1

Sequence 1, Application US/090793

Patent No. 6140486

GENERAL INFORMATION:

APPLICANT: Calgene, Inc.

TITLE OF INVENTION: Production of polyunsaturated fat

US-09-090-793-1

```

1 TITLE OF INVENTION: POLYKETIDE LIKE SYNTHESIS GENES IN PLANTS
2
3 FILE REFERENCE: GENE 131-01US
4
5 CURRENT APPLICATION NUMBER: 08/09/090,794
6
7 CURRENT FILING DATE: 1998-06-04
8
9 EARLIER APPLICATION NUMBER: E2/949,650
10
11 EARLIER FILING DATE: 1997-06-04
12
13 NUMBER OF SEQ ID NOS: 66
14
15 SOFTWARE: Patcut in Ver. 2.0
16
17 SEQ ID NO: 1
18
19 LENGTH: 37895
20
21 TYPE: DNA
22
23 ORGANISM: Shewanella putrefaciens
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25 US 09-090-794-1
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Seq Sequence 370 BP: 126 A; 73 C; 82 G; 89 T; 0 other;

Query Match Best Local Similarity 100.0%; Score 21; FR 10; Length 370;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 113 ATAAATCACCACCTGTGCA 133

DB 120 ATAAATCACCACCTGTGCA 140

RESULT 15

AA68870
ID AAC68870 standard; DNA: 375 BP.

XX AAC68870;

XX 25-FEB-2001 (first entry)

XX Modified human Interleukin 5 coding sequence SEQ ID NO: 33.

XX Asthma; IL-5; Interleukin 5, alpha; cytokine; helminthic infection;

XX cancer; eosinophilia; vaccine; allergic rhinitis; ds.

XX Homo sapiens.

XX Clostridium tetani.

XX WO200065058-A1.

XX 02-NOV-2000.

XX 19-APR-2000; 2000W0-DK00205.

XX 23-APR-1999; 99DK-0000552.

XX 06-MAY-1999; 99DS-0132811.

XX (METH-) M & E BIOTECH AS.

XX Klyner S;

XX WI1: 2000-672791/65.

XX P-PSDB: AAB45517.

XX Disclosure: Page 143-144; 172pp; English.

XX The present invention is concerned with methods of treating asthma,

XX eosinophilia, allergic rhinitis and other allergic diseases. These

XX involve the use of Interleukin-5 (IL-5) analogues and modified IL-5

XX proteins and their coding sequences to down-regulate IL-5 activity and

XX thus reduce eosinophil numbers. The allergic diseases may be treated

XX using autoantibodies, nucleic acid vaccines or live vaccines. In addition,

XX it is possible that they may be used in the treatment of cancer and

XX helminthic infections.

XX Sequence 375 BP: 130 A; 82 C; 78 G; 85 T; 0 other;

XX Query Match Best Local Similarity 6.1%; Score 21; DB 21; Length 375;

XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX UY 113 ATAAATCACCACCTGTGCA 133

XX DB 113 ATAAATCACCACCTGTGCA 133

Search completed: November 7, 2002, 22:02:43

Job time: 93.2861 secs



[illegible][illegible]

BASE COUNT 280 A 148 C 171 G 239 T
 ORIGIN

Query Match 8.78; Score 30; DB 4; Length 848;
 Best Local Similarity 100.0%; Pred. No. 4, 1e-05;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

107 TCAATGTCGCTTATTAACACAGATT 136
 640 TCAATGTCGCTTATTAACACAGATT 411

RESULT 15
 AF294756 405 bp mRNA linear PRI 10 MAY 2002
 LOCUS Saimiri sciureus interleukin 5 mRNA, complete cds.
 DEFINITION AF294756
 ACCESSION AF294756.1 GI:15213529
 VERSION
 KEYWORDS
 SOURCE Saimiri sciureus.
 ORGANISM Saimiri sciureus.
 Eukaryota; Mammalia; Chordata; Primates; Platyrrhini; Cebidae; Cebinae;
 Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae;
 Saimiri.

REFERENCE 1 (bases 1 to 405)

AUTHORS

TITLE

ABSTRACT

KEYWORDS

IDENTIFICATION

PROTEIN

FUNCTION

REFERENCES

NOTES

COMMENTS

REMARKS

ADDITIONAL

FEATURES

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Search completed: November 7, 2002, 21:39:52
 Job time: 979.587 secs


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61 CTCTGACGTCGACCTTCCTCCGACACACCTTTTTCGCTCTATGTCCTT 120
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RESULTS

AAZ55546 standard: cDNA: 610 bp.

AAZ55546:

14-MAR-2000 (first entry)

canine interleukin-5 (IL-5) cDNA.

Interleukin-5 (IL-5) antibody: canine; inhibitor; immune response;

immunological; tumor; cancer; autoimmune disease; vaccine; ss;

canine; familiar;

canine; interleukin-5 (IL-5) cDNA.

canine; interleukin-5 (IL-5) cDNA.

canine; interleukin-5 (IL-5) cDNA.

canine; interleukin-5 (IL-5) cDNA.

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canine; interleukin-5 (IL-5) cDNA.

canine; interleukin-5 (IL-5) cDNA.

can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used to detect, and in drug targeting.

Sequence 610 bp; 202 A; 114 C; 149 G; 156 T; 0 other

Query Match

Best Local Similarity 100.0%; Score 495; 1482; Length 610;

Mismatch 345; Gap 0; Mismatch 0; InPct 0; Gaps 0;

61 CTCTGACGTCGACCTTCCTCCGACACACCTTTTTCGCTCTATGTCCTT 120

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RESULTS

AAZ55547 standard: cDNA: 610 bp.

AAZ55547:

14-MAR-2000 (first entry)

canine interleukin-5 (IL-5) cDNA complement.

Interleukin-5 (IL-5) antibody: canine; inhibitor; immune response;

immunological; tumor; cancer; autoimmune disease; vaccine; ss;

canine; familiar;

canine; interleukin-5 (IL-5) cDNA.

canine; interleukin-5 (IL-5) cDNA.

canine; interleukin-5 (IL-5) cDNA.

canine; interleukin-5 (IL-5) cDNA.

canine; interleukin-5 (IL-5) cDNA.

canine; interleukin-5 (IL-5) cDNA.

canine; interleukin-5 (IL-5) cDNA.

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canine; interleukin-5 (IL-5) cDNA.

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canine; interleukin-5 (IL-5) cDNA.

canine; interleukin-5 (IL-5) cDNA.

canine; interleukin-5 (IL-5) cDNA.

canine; interleukin-5 (IL-5) cDNA.

canine; interleukin-5 (IL-5) cDNA.

Seq: Sequence: 479 bp; 129 A; 73 G; 82 C; 89 T; 9 other:

Query Match: 6.1%; Score 21; DB 10; Length 470;

Host Local Similarity: 100.0%; Prod. No. 0.87; Mismatches: 0; Gaps: 0;

Matches: 21; Conservative: 0; Models: 0; Gaps: 0;

21 137ACACAGTGGTATTTTAT 233

140 TGTACAGTGGTATTTTAT 120

RESULT 15

AA66870/

10 AA66870 standard; DNA; 475 bp;

XX AA66870;

XX 26-FEB-2001 (first entry)

XX Modified human Interleukin 5 coding sequence SEQ ID NO: 44.

XX Asthma: IL-5, interleukin-5, allergic cytokine; hematinic infection;

XX cancer; eosinophilic; varicose; allergic rhinitis; ds.

XX Homo sapiens.

XX restriction endon.

XX W020065656 A1

XX 02 NOV 2000.

XX 19-APR-2000; 20006-1K00205.

XX 24 APR-1999; 990K-0000552.

XX 06 MAY-1999; 990S-0132811.

XX (M331-) M & E BIOTECH AS.

XX K15808 S;

XX W01: 2000-07-27/1/65.

XX P-1808; AAA45517.

XX down-regulating interleukin 5 (IL-5) activity in humans by

XX administering IL-5 and/or an IL-5 analogue, useful in the treatment,

XX prophylaxis or amelioration of asthma or other chronic allergic

XX condition;

XX Disclosure: Page 143-144; 172pp; English.

XX The present invention is concerned with methods of treating asthma,

XX eosinophilia, allergic rhinitis and other allergic diseases. These

XX involve the use of interleukin-5 (IL-5) analogues and modified IL-5

XX proteins and their coding sequences to down-regulate IL-5 activity and

XX thus reduce eosinophil numbers. The allergic diseases may be treated

XX using anti-viral, nucleic acid, or protein or two gene seq. In addition,

XX it is possible that they may be used in the treatment of cancer and

XX helminthic infections

XX Sequence: 475 bp; 130 A; 82 G; 78 C; 85 T; 9 other:

Query Match: 6.1%; Score 21; DB 21; Length 475;

Host Local Similarity: 100.0%; Prod. No. 0.87;

Matches: 21; Conservative: 0; Mismatches: 0; Gaps: 0;

21 137ACACAGTGGTATTTTAT 233

140 TGTACAGTGGTATTTTAT 113

Search completed: November 7, 2002, 22:02:44

Job time: 93.2861 secs



LENGTH: 816
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-755-633-2

Query Match
 Best Local Similarity: 5.1%; Score 21; DB 2; Length 816;
 100.0%; Pred. No. 0.26;
 Matches: 21; Conservative: 0; Mismatches: 0; Indels: 0;

42 212 CTTGAGGTAGCTAGGAA 60
 |||
 146 214 TGGACAGGTAGCTAGGAA 19

RESULT 4
 US-09-755-633-2
 Sequence 19; Application PC/1096410957
 GENERAL INFORMATION:
 APPLICANT: Goldstein, Harris, Kollman, Tobias K.
 TITLE OF INVENTION: Immunofluorescent Mouse Models of
 TITLE OF INVENTION: Pathogenesis of human disease and efficacy and toxicity of
 TITLE OF INVENTION: Disease treatments
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Law Office of Sherman and Shalloway
 STREET: 412 N. Washington Street
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5 1/4 inch, and 4.8 floppy
 COMPUTER: IBM clone, 8088 Turbo
 OPERATING SYSTEM: MS DOS 5.0
 SOFTWARE: Word Perfect, Version 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PC/1096410957
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Richard A. Steinberg
 REGISTRATION NUMBER: 26,588
 TELEPHONE: (703) 549-2282
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 549-2282
 TELEFAX: (703) 886-0106
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 nucleotides
 TYPE: nucleic acid
 STRATEGY: 5'-3'-
 TOPLOGY: Linear
 MOLECULE TYPE: cDNA
 HYPOHELYTAL: no
 ORIGINAL SOURCE:
 ORGANISM: human
 FEATURES:
 NAME/FEATURE: 11-6
 PC/1096410957 19

Query Match
 Best Local Similarity: 5.5%; Score 19; DB 5; Length 29;
 100.0%; Pred. No. 2.8;
 Matches: 19; Conservative: 0; Mismatches: 0; Indels: 0;

42 212 CTTGAGGTAGCTAGGAA 60
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 146 214 TGGACAGGTAGCTAGGAA 19

RESULT 4
 US-09-755-633-2
 Sequence 78; Application US/09280799
 Patent No. 6166603

GENERAL INFORMATION:
 APPLICANT: Dean, Nicholas M.
 APPLICANT: Kattas, James G.
 APPLICANT: McKay, Robert
 TITLE OF INVENTION: ANTIGEN MODULATION OF INTERLEUKIN 5 SIGNAL
 TITLE OF INVENTION: TRANSCRIPTION
 FILE REFERENCE: ISPH-0340
 CURRENT FILING DATE: 1996-04-26
 NUMBER OF SEQ ID NOS: 208
 SOFTWARE: Patent In Vot. 2.0
 SEQ ID NO: 78
 LENGTH: 3230
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-755-633-78

Query Match
 Best Local Similarity: 5.5%; Score 19; DB 3; Length 3230;
 100.0%; Pred. No. 2.4;
 Matches: 19; Conservative: 0; Mismatches: 0; Indels: 0;

42 CTTGAGGTAGCTAGGAA 60
 |||
 146 2172 CTTGAGGTAGCTAGGAA 2154

RESULT 5
 US-09-755-633-78
 Patent No. 5924640
 APPLICANT: Benito, Jasob, Takas, Kyriaki, Sotirios, Eva
 TITLE OF INVENTION: HUMAN B CELL DIFFERENTIATION FACTOR AND
 PROCESS OF INVENTION: SAID FACTOR
 NUMBER OF SEQUENCES: 2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-09-755-633-78
 FILING DATE: 21 SEP 1987
 SEQ ID NO: 1
 LENGTH: 3230
 5924640 1

Query Match
 Best Local Similarity: 5.5%; Score 19; DB 5; Length 3230;
 100.0%; Pred. No. 2.4;
 Matches: 19; Conservative: 0; Mismatches: 0; Indels: 0;

42 CTTGAGGTAGCTAGGAA 60
 |||
 146 2172 CTTGAGGTAGCTAGGAA 2154

RESULT 6
 US-09-755-633-78
 Sequence 48; Application US/08621841
 Patent No. 6056869
 GENERAL INFORMATION:
 APPLICANT: Statist, Margaret A.
 TITLE OF INVENTION: TREATMENT OF EARLY MAINTAIN ASSOCIATED
 TITLE OF INVENTION: LESIONS
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Fisher, Holbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent In Review #1.0; Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-09-755-633-78

1 Topology: Linear
2 FEATURE:
3 NAME: 755-633-11
4 LOCATION: M...1111
5 OTHER INFORMATION:
6 US-09-755-633-11

Query Match 4.9% Score 17: DB 2: Length 1272:
Best Local Similarity 100.0% Pred. No. 24:
Matches 17: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 160 CCGGCGGAGATTGAT 176
11111111111111111111
DB 415 CCGGCGGAGATTGAT 431

RESULT 10
US-09-755-633-11
1 Sequence 32: Application US/09318448
2 Patent No. 62:0950
3 GENERAL INFORMATION:
4 APPLICANT: Johnson, William G.
5 APPLICANT: Stevens, Edward S.
6 TITLE OF INVENTION: METHOD FOR OBTAINING PREVENTING AND TREATING
7 TITLE OF INVENTION: PHYSIOLOGICAL DISORDERS
8 FILE REFERENCE: 603-1-067
9 CURRENT ATTACHEE NUMBER: 09-0778-435
10 CURRENT FILING DATE: 1999-05-25
11 NUMBER OF SEQ ID NOS: 46
12 SOFTWARE: Patented Ver. 2.0
13 SEQ ID NO 42
14 LENGTH: 1547
15 TYPE: DNA
16 ORGANISM: Homo sapiens
17 US-09-318-448-42

Query Match 4.9% Score 17: DB 4: Length 1547:
Best Local Similarity 100.0% Pred. No. 23:
Matches 17: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 227 TTTTATTTTCAGACT 243
11111111111111111111
DB 602 TTTTATTTTCAGACT 586

RESULT 11
US-09-023-023-1
1 Sequence 32: Application US/09023023
2 Patent No. 6121018
3 GENERAL INFORMATION:
4 APPLICANT: Kistling, Ray Kelly
5 TITLE OF INVENTION: Intellectual Property Rights for
6 NUMBER OF SEQUENCES: 2
7 CORRESPONDENCE ADDRESS:
8 ADDRESS: 2000 S. 1st Street
9 STREET: 2000 S. 1st Street
10 CITY: Kind of Prussia
11 STATE: PA
12 COUNTRY: USA
13 ZIP: 19406
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Diskette
16 COMPUTER: IBM compatible
17 OPERATING SYSTEM: DOS
18 SOFTWARE: FASTSeq for Windows Version 2.0
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: 05/023-023-1
21 FILING DATE: 12-FEB-1998
22 CLASSIFICATION:
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 00/0422-030
25 FILING DATE: March 27, 1997
26 AUTOMATED/AGENT INFORMATION:

1 NAME: Hans, William T
2 REGISTRATION NUMBER: 44-444
3 REGISTRATION NO. NUMBER: 44-444
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 610-270-5219
6 TELEFAX: 610-270-5090
7 TELEEX:
8 INFORMATION FOR SEQ ID NO: 1:
9 SEQUENCE CHARACTERISTICS:
10 LENGTH: 2071 base pairs
11 TYPE: nucleic acid
12 STRANDEDNESS: single
13 TOPOLOGY: linear
14 US-09-023-023-1

Query Match 4.9% Score 17: DB 4: Length 2071:
Best Local Similarity 100.0% Pred. No. 24:
Matches 17: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 224 GCGATTATTTTCAG 239
11111111111111111111
DB 1219 GCGATTATTTTCAG 1204

RESULT 12
US-09-453-702B-96/A
1 Sequence 32: Application US/09453702B
2 Patent No. 6365724
3 GENERAL INFORMATION:
4 APPLICANT: Bialletti, Frederick R.
5 APPLICANT: Bernal, Nicole L.
6 APPLICANT: Bialletti, Rod
7 TITLE OF INVENTION: NO. 6365724-1 Sequences of E. coli 0157
8 NUMBER OF SEQUENCES: 265
9 CORRESPONDENCE ADDRESS:
10 ADDRESS: 3041 S. Brady
11 STREET: 3041 S. Brady
12 CITY: Madison
13 STATE: WI
14 COUNTRY: US
15 ZIP: 53701-2113
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Diskette
18 COMPUTER: IBM pc compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Word Perfect 8.0
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09453702B
23 FILING DATE: 01 Dec 1999
24 CLASSIFICATION: Unknown
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 60/110,955
27 FILING DATE: 04 Dec 1998
28 AUTOMATED/AGENT INFORMATION:
29 NAME: Seely, Nicholas J.
30 REGISTRATION NUMBER: 27486
31 REGISTRATION NO. NUMBER: 27486
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (608) 271-5600
34 TELEFAX: (608) 271-9166
35 INFORMATION FOR SEQ ID NO: 96:
36 LENGTH: 34063
37 TYPE: nucleic acid
38 STRANDEDNESS: double
39 TOPOLOGY: linear
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 34063
42 TYPE: nucleic acid
43 STRANDEDNESS: double
44 TOPOLOGY: linear
45 MEDIUM TYPE: DNA (genomic)
46 SOFTWARE: DESCRIPTION: SEQ ID NO: 96:
47 US-09-453-702B-96

Query Match 4.9% Score 17: DB 4: Length 34063:

Best local similarity: 300.0% (Seq. No. 21)
Matches: 17; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 217 CACTGCTGATTTAT 233
|||||

DB 3249 CACTGCTGATTTAT 3233

RESULT 13

US-06-375-709-1/c

Sequence 1, Application US/08375709

Patent No. 5684898

GENERAL INFORMATION:

APPLICANT: YAZAWA, Kazuaki

APPLICANT: YAMADA, Atsushi

APPLICANT: KATO, Satoshi

APPLICANT: KONO, Kiyoshi

TITLE OF INVENTION: Gene Coding For Elcosapentaenoic Acid

TITLE OF INVENTION: Synthesizing Enzyme and Process for Production of

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESS: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/06/375-709

FILING DATE: 20 JAN 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/178,251

FILING DATE: 14 MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 4 147945

FILING DATE: 15-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold G

REGISTRATION NUMBER: 25,258

REFERENCE: 435-709-1/c

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)572-5390

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 37895 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Shearwater patrefactions SCRC 2874 (FERM

US-08-375-709-1

Query Match: 4 3% Score 17; DB: 1; Length: 37895;

Best local similarity: 100.0%; Pred. No. 21;

Matches: 17; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 15 ACTGCTGTTATACA 31
|||||

DB 1211 ACTGCTGTTATACA 1195

RESULT 14

US-09-755-633-1/c

Sequence 1, Application US/09-755-633-1/c

Patent No. 5798259

GENERAL INFORMATION:

APPLICANT: YAZAWA, Kazuaki

APPLICANT: YAMADA, Atsushi

APPLICANT: KATO, Satoshi

APPLICANT: KONO, Kiyoshi

TITLE OF INVENTION: Gene Coding For Elcosapentaenoic Acid

TITLE OF INVENTION: Synthesizing Enzyme and Process for Production of

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESS: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/755-633-1/c

FILING DATE: 20 JAN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/178,251

FILING DATE: 14 MAY-1993

APPLICATION NUMBER: JP 4 147945

FILING DATE: 15 MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold G

REGISTRATION NUMBER: 25,258

REFERENCE: 435-709-1/c

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)572-5390

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 37895 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Shearwater patrefactions SCRC 2874 (FERM

US-08-755-633-1

Query Match: 4 3% Score 17; DB: 1; Length: 37895;

Best local similarity: 100.0%; Pred. No. 21;

Matches: 17; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 15 ACTGCTGTTATACA 31
|||||

DB 1211 ACTGCTGTTATACA 1195

RESULT 15

US-09-090-793-1/c

Sequence 1, Application US/09-090-793-1/c

Patent No. 6140486

GENERAL INFORMATION:

APPLICANT: Calgene, Inc.

TITLE OF INVENTION: Production of polyunsaturated

```

: TITLE OF INVENTION: polynucleotide like synthesis genes in plants
: FILE REFERENCE: GENE.131.01US
: CURRENT APPLICATION NUMBER: 08/702,090, 793
: CURRENT FILING DATE: 1998-06-04
: EARLIER APPLICATION NUMBER: 62/348,650
: EARLIER FILING DATE: 1997-06-04
: NUMBER OF SEQ ID NOS: 66
: SOFTWARE: Patonlin Ver. 2.0
: SEQ ID NO: 1
: LENGTH: 37895
: TYPE: DNA
: ORGANISM: Shewanella putrefaciens
: US-09-090-793-1

Query Match      4.9%  Score 17; DB 3; Length 37895;
Host Local Similarity 100.0%; Prod. No. 21;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AATTGGTGTATTTACA 31
    |||
Db 1211 ACTGGTGTATTTACA 1195

```

Search completed: November 8, 2002, 06:11:38
 Job time : 41.505 secs

	ORGANISM
	Mus musculus
FEATURES	Enzyme: Mgfz9; Chromid; Cranial; Vertebral; Embryonic; Mammary; Embryo; Rodentia; Sciurognathi; Muridae; Murine; Mus.
REFERENCE	1 (bases 1 to 441)
AUTHORS	Maria,M., Billiet,L., Allen,M., Bowles,M., Dietrich,N., Dubnue,T., Gotsch,S., Kuchta,J., Lacy,M., Le,M., Martin,d., Morris,M., Schell-leberich,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Heston,B., Wylie,T., Lemon,G., Soares,B., Wilson,R., and Watson,R.
TITLE	The MashU-HIMI Mouse EST project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Maria M/mouse_est_project@washington.washington.edu Washington University School of Medicine 4444 Forest Park Parkway, box B501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through the IMAG Consortium (info@image.llnl.gov) for further information. M1:991172 Seq primer: -28M's rcv2 from AmerSham High quality sequence stop: 420. Location/Qualifiers 1..441

BASE COUNT	112 a	95 c	109 g	115 t
ORIGIN				
Query Match:		5.8%	Score 209	DB %
Best Local Similarity	100.0%		Prod. No. 1.6e-02	
Matches	209	Conservative	2	Mismatches 0
				Indels 0
				Gaps 0
QY	111	TCGTCCTTTTATTAAAC	130	TTTTTTTTTTTTTTTT
DB	654	TGTCCTTTTATTAAAC	473	
RESULT 5				
AC677395/3				
LOCUS	AC677395			
DEFINITION	HS-5526-AL-G11-17A HGP-11 human male MAC Library Homo sapiens			
ACCESSION	U000000000			
VERSION	AC677395.1			
KEYWORDS	Genomic clone			
SOURCE	GenBank			
ORGANISM	Homo sapiens			
	Human			
	Popkay, M. et al. (1993) Characterization of Vertebrate Endothelium; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
REFERENCE	1 (bases 1 to 528)			
AUTHORS	Mahites, R. et al. Wallace, J. C., Smith, K., Swartz, S., Helman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M. D., and Hood, L.			
TITLE	Sequence-tagged connectors: A sequence approach to mapping and			

JOURNAL
MEDLINE
COMMENT

99380089
Proc Natl Acad Sci U S A. 96 (17): 10000-10004.
Contact: Melbaire M. Wallace, Jr., Head of
High Throughput Sequencing Center
University of Washington
401 Groves Ave. Room N-110, Seattle, WA
Tel: (206) 616 9639
Fax: (206) 616 4007
Email: jwallace@u.washington.edu
Clones are deposited in the human genome
library and indexed by Enzygnis contact: Peter
(peter@u.washington.edu) or E. Chen in
BAC/AC Resourc. at the F-/BAC/Resour. at the
or from Resour. at the F-/BAC/Resour. at the
<http://www.hfsc.washington.edu>
Plasmid: 1102 (2x) M. Wallace, Jr.
Seq primer: 17
Class: BAC clone
High quality sequence of 4.5 kb.
Location/Qualities
1. 100%

[illegible]

	SEQUENCE	1.. 476 /c=human "Acanthopis lepus" /db_xref "taxon:8455" /clone-"MAE:3055645" /clone-11b "NIDHO XRC 001" /sex-"female" /lab host "mignon (Phage-resistant)" /note "Organism query: Vector: PCMV SHORTR; SITE 1: NOTL; SITE 2: SALL; cloned unidirectionally, primer oligo dT average insert size 2.0 kb. Constructed by life technologies."			
BASE COUNT	120 a	61 c	62 g	133 t	
ORIGIN					
Query Match	5.5%	Score: 19	DP: 12	Length: 476	
Post Local Similarity	100.0%	Prod. No.	4.6e+02		
Matches	19	Conservative	0	Mismatches	0
				Indels	0
				Gaps	0
QY	118 TTTATTAAAGATCAATT 146				
120	TTTTTAAGACACATTT 51				
RESULT 14					
A0462483/c					
LOCUS	H5_5213.A1.A08.SP6.RPCL11 Human Male BAC library Homo sapiens	389 bp	ENA	Linear	GEN 24-APR-1990
DEFINITION	genomic clone plasmid pGEM 704.0315 pGM A, DNA sequence.				
VERSION	A0462483				
KEYWORDS	A0462483.1 ct-46.65254				
SOURCE	DSB.				
ORGANISM	Human.				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrates; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
REFERENCE	1 (bases 1 to 489)				
AUTHORS	Maharaj G.C., Wallace J.C., Smith P.V., Scottell L.S., Holman T.J., Koller A., Shaker R., Portland D., Young T.T., Zhou S., Adams M.D. and Hood L.				
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)				
MEDLINE	99380589				
COMMENT	Contact: Maharaj G.C., Wallace J.C., Hood L. High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel.: (206) 616-4618 Fax: (206) 616-4887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RP11-11. For BAC library availability, please contact Peter de Joux (pjederde@alum.mit.edu/butler@du). Clones may be purchased from BACDAC Resources (http://tcf.fri.uni-bielefeld.de/bacdac/) or from Research Technologies (Inforesgen.com) BAC end Web Service: http://www.btc-genetics.com Plasmid: 789 row: A column: 15 Seq primer: SP6 Class: BAC ends High quality sequence: steps: 489, Location/Qualifiers 1.. 389 /organism "Homo sapiens" /db_xref "taxon:9606" /clone-Plate: 789 Tol-15 Row-A" /clone-11b "RPCL11 Human Male BAC Library" /seq-map /contig="overlapped: 99A063.6 site 1; 99C01.2; 99C01.3; Male blood DNA was isolated from one randomly chosen donor and partially digested with 2 combinations of EcoRI and EcoRV-MspI/HaeIII. Size selected DNA was ligated into the pBR322.6 vector at EcoRI sites"				
FEATURES					
SOURCE					
BASE COUNT	182 a	56 c	56 g	95 t	

[illegible]

Fri Nov 8 12:51:08 2002

us-09-755-633-11.rst

Page 8

Job time : 640.537 secs

[illegible][illegible][illegible]

[illegible]

RESULT 12				
AX083948/c	AX083948	343	PC	RNA
LOCUS	Sequence 10	From Patent WO011049.		
DEFINITION	AX083948			
ACCESSION	AX083948.1			
VERSION	GI:13185507			
				FAT 24-FPP-2003

ORGANISM	Canis familiaris
REFERENCE	Eukerkyt's, Mett's, Chelid's, Fud's, Velleid's, Eteleustomi,
AUTHORS	Mammalia: Eutheria; Carnivora: Fissipedia; Canidae; Canis.
TITLE	1 (bases 1 to 343)
JOURNAL	Sho, H., Lawton, R., Mettrey, B. and Aiyappa, A. P.
FEATURES	Methods and compositions concerning canine interleukin 5
SOURCE	Patent: WO 011049-A 10 15-FEB-2001; INDEX LABORATORIES, INC. (US)
	Location/Qualifiers
	1..343
	/organism="Canis familiaris"
BASE COUNT	114 a 71 c 76 g 82 t
ORIGIN	40; xref="taxon:675"

	Query Match	72.5%	Score 250	EB 67	Length 343
Best Local Similarity	100.0%		Pred. No. 3.8e-57		
Matches 250	Conservative	0	Mismatches	0	Indels
		0		0	Gaps

[illegible]

RESULT 13	AF294756	405 bp	1100-2	PR1 10-MAY-2002
AF294756/c				
LOCUS	Salmonella	interleukin-5	mRNA, complete cds.	
DEFINITION	Salmonella	interleukin-5	mRNA, complete cds.	
ACCESSION	AF294756			

VERSION	AF294456.1	GI:1524629
KEYWORDS	Saimiri sciureus.	
SOURCE	Saimiri sciureus.	
ORGANISM	Saimiri sciureus	
REFERENCE	Eklavya et al. 2004. The data of Granular V. Mammalia. Furthering Primates; plaything Samiti.	
AUTHORS	1 (bases 1 to 400)	
TITLE	Harad T.M., Eklavya A. and Kazan J.M. Molecular cloning, characterization, and monkey (Saimiri sciureus) 101 and 102 (2004) 1197-1223	
JOURNAL	Journal of Molecular Biology	
MEDLINE	11976788	
PUBMED	2 (bases 1 to 400)	
REFERENCE	Harad T.M., Eklavya A. and Kazan J.M. Direct Submission	
AUTHORS	Submitted (05-003-2004) for phylogeny. The	
TITLE	Gyane, 23, Avenue Pasteur, Cayenne 97306,	
JOURNAL	Location/Qualities	
FEATURES	1..405	
SOURCE		

Query Match	Score	Size	Def
Best Local Similarity	81.07%	Prod. 230,557	
Matches: 275	Conservation: 0%	MSMAChDS: 44%	

[illegible]

RESULT	14
CEYINF5A/C	
LOCUS	CEYINF5A
DEFINITION	Cerecoccus forquatus 435 bp
ACCESSION	L26033
VERSION	L26033.1
KEYWORDS	C125143.9
SOURCE	Interleukin 5
ORGANISM	Cerecoccus forquatus (individual isolate) & Cerecoccus forquatus


```

|||||
Db 61 CTTGTGACGTCTGATCTTTGTGTCACAACTTTTTHHGGGCGCTGATAGTGTCTT 120
QY 121 TATTAAACACAACTTTTGCAATCTTATGCAACAGCGCGCGGTGTGTACCTTGTCTT 180
Db 121 TATTAAACACAACTTTTGCAATCTTATGCAACAGCGCGCGGTGTGTACCTTGTCTT 180
QY 181 CATCTCTGTATACCTGAAAGCTTGTATAGTCACACCTGTGTATCTTGTATGATG 240
Db 181 CATCTCTGTATACCTGAAAGCTTGTATAGTCACACCTGTGTATCTTGTATGATG 240
QY 241 ACTAATGATATCACTTTGTGATGCTTATGATGATGATGATGATGATGATGATG 300
Db 241 ACTAATGATATGATGCTTGTGATGCTTATGATGATGATGATGATGATGATGATG 300
QY 301 CAAGTCTGTGCGACGAGCTATGATGAGATTTTGTACAGCAAA 345
Db 401 CAAGTCTGTGCGACGAGCTATGATGAGATTTTGTACAGCAAA 345

RESULT 5
AAZ55546/c
ID AAZ55546 standard; cDNA; 610 bp.
XX
AC AAZ55546;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-5 (IL-5) cDNA.
XX
KW Interleukin-5; IL-5; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT CDS 29..433
FT /tag = a
FT /product = "Canine IL-5"

W09961618-A2
PD 02-DEC-1999.
XX
PF 28 MAY 1999. 99W0-DS11942.
XX
PP 29-MAY-1998. 98WS-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Drellz MJ, Wonderling RS;
XX
DR WPI: 2000-072623/06.
DR P-PSDB: AAY58219.
XX
PI Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PI useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 1b; Page 223 224; 264pp; English.
XX
CC Sequences AAZ55546, 255551 represent cDNA sequences encoding
CC canine interleukin 5 (IL-5). The invention relates to canine
CC IL-4, canine or feline Fcγ-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-α (IFN-α), and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumors, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences

```

can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used in detection, and in drug targeting.

Sequence 610 bp, 302 A, 114 C, 139 G, 155 T, 6 other;

Query Match 100.0%; Score 345; E= 21; Length 610;

Best Local Similarity 100.0%; Pred. No. 2,7e-93;

Matching 345, Conserved Atoms 0; Mismatches 0; Indels 0; Gaps 0;

```

27 1 AATTTGGGCGGCTGATCTTTGTGTCACAACTTTTTHHGGGCGCTGATAGTGTCTT 60
Db 430 AATTTGGGCGGCTGATCTTTGTGTCACAACTTTTTHHGGGCGCTGATAGTGTCTT 60
QY 61 CTTGTGACGTCTGATCTTTGTGTCACAACTTTTTHHGGGCGCTGATAGTGTCTT 120
Db 370 CTTGTGACGTCTGATCTTTGTGTCACAACTTTTTHHGGGCGCTGATAGTGTCTT 311
QY 121 TATTAAACACAACTTTTGCAATCTTATGCAACAGCGCGCGGTGTGTACCTTGTCTT 180
Db 310 TATTAAACACAACTTTTGCAATCTTATGCAACAGCGCGCGGTGTGTACCTTGTCTT 251
QY 181 CATCTCTGTATACCTGAAAGCTTGTATAGTCACACCTGTGTATCTTGTATGATG 240
Db 250 CATCTCTGTATACCTGAAAGCTTGTATAGTCACACCTGTGTATCTTGTATGATG 191
QY 241 ACTAATGATATCACTTTGTGATGCTTATGATGATGATGATGATGATGATGATG 300
Db 150 ACTAATGATATGATGCTTGTGATGCTTATGATGATGATGATGATGATGATGATG 131
QY 301 CAAGTCTGTGCGACGAGCTATGATGAGATTTTGTACAGCAAA 345
Db 130 CAAGTCTGTGCGACGAGCTATGATGAGATTTTGTACAGCAAA 86

RESULT 6
AAZ55547
ID AAZ55547 standard; cDNA; 610 bp.
XX
AC AAZ55547;
XX
DT 14 MAR 2000 (first entry)
XX
DE Canine interleukin 5 (IL 5) cDNA complement.
XX
KW Interleukin 5; IL 5; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT CDS 178..582
FT /tag = a
FT /product = "Canine IL-5"

W09961618-A2
PD 02-DEC-1999.
XX
PF 28 MAY 1999. 99W0-DS11942.
XX
PP 29-MAY-1998. 98WS-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Drellz MJ, Wonderling RS;
XX
DR WPI: 2000-072623/06.
DR P-PSDB: AAY58219.
XX

```


KW antisense oligonucleotide; allergic rhinitis; inflammatory skin diseases
 XX allergic conjunctivitis; inhibitor; SS.
 XX Homo sapiens.
 XX US6048726 A.
 XX 11-APR-2000.
 XX 15-MAY-1998; 9805-0079839.
 XX 15-MAY-1998; 9805-0079839.
 XX (WELT/?) WEIMAN J.
 XX (KARL/?) KARIM A S.
 XX Wetman JR. Serum AS.
 XX WPI: 2009 402754/26.
 XX 01-oligonucleotide comprising non-natural internucleoside linkage, useful
 P1 for inhibiting interleukin-5 expression and treating inflammatory
 P1 diseases, asthma, allergic rhinitis, allergic conjunctivitis.
 XX Disclosures: Column 3-4; 11pp; English.
 XX This sequence represents the human interleukin-5 (IL-5) encoding
 CC nucleotide sequence. Interleukin-5 is involved in eosinophilic
 CC inflammation and inflammatory disorders. The present invention relates
 CC to an IL-5 antisense oligonucleotide (see AAI3337) which inhibits the
 CC expression of IL-5. The antisense oligonucleotide has a least one
 CC non-natural internucleoside linkage. The oligonucleotide is able to
 CC inhibit IL-5 secretion in a dose dependent manner, and is useful for
 CC inhibiting IL-5 expression and therefore treating inflammatory diseases,
 CC asthma, allergic rhinitis, allergic conjunctivitis and inflammatory skin
 CC diseases such as eczema.
 XX Sequence 816 BP; 277 A; 147 G; 164 G; 218 T; 0 other;
 SU Query Match 67.1%; Score 231.4; H: 21; Len: h 816;
 Best local Similarity 80.4%; Pred. No. 2,796-59;
 Matches 271; Conserved: 0; Mismatch: 66; Indels: 0; Gaps: 0;
 1 ATTTCGAGTGTGCACTGATGTTTATATACACCAAGAAATCTGCAGCTATAGCA 60
 446 ATTTCGATATATACCACTGATGTTTATATACACCAAGAAATCTGCAGCTATAGCA 387
 61 CTTTGATCTGCACTGATGTTTATATACACCAAGAAATCTGCAGCTATAGCA 120
 386 TGGGTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 327
 121 TATTAACACAGCTTTTATTAAGTTTATGCAACAGCTGCTGCTGCTGCTGCTGCT 180
 326 TATTAACACAGCTTTTATTAAGTTTATGCAACAGCTGCTGCTGCTGCTGCTGCT 267
 181 CAATGCTATAGCTGCAACAACTCTTATTAAGCTGCTGCTGCTGCTGCTGCTGCT 240
 266 CATTGCTATAGCTGCAACAACTCTTATTAAGCTGCTGCTGCTGCTGCTGCTGCT 207
 241 ATTAAATATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 206 AATAGCAATCTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 147
 301 CAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 347
 146 CAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 110

RESULT 14
 AAA34857/..
 11 AAA34857 standard; ENA; 816 BP.
 XX
 AC AAA34857;

XX 28-JUL-2000 (first publ.)
 XX Human adenovine receptor; a novel polynucleotide;
 XX Human adenovine receptor; a novel polynucleotide;
 XX Phosphorothioate; improved respiratory inhibitor;
 KW allergic disease; bronchoconstriction inhibitor;
 KW antiallergic; antipneumonia; cytostatic; analgesic;
 KW lung disease; ischemic condition; pulmonary disease;
 KW respiratory distress syndrome; cystic fibrosis;
 KW pulmonary hypertension; and obstructive pulmonary
 KW cancer; leukemia; lymphoma; myeloid metaplasia;
 XX Homo sapiens.
 XX WCI06007525 A2.
 XX 24-FEB-2000.
 XX 03-AUG-1999; 99W 532 114.
 XX 03-AUG-1998; 9805 402754/26.
 XX (DYER/?) UNIV EAST CAROLINA.
 XX Nyeo JW.
 XX WPI: 2009 205671/18.
 XX Nex antisense oligonucleotides useful for treating
 PT vasoconstriction, inflammation, allergies, asthma
 PT bronchitis, emphysema, respiratory distress synd
 PT cancers.
 XX Disclosures: Page 716; 14 pp; English.
 XX The present invention describes a new composition
 CC antisense oligonucleotide (N) with low adverse
 CC targets nucleotide sequence and bronchoconstrictor
 CC inflammation. The CN can have an inflammatory
 CC antiallergic, cytostatic and analgesic activity
 CC useful for the treatment of diseases associated w
 CC impaired airways, including lung disease and disor
 CC effects afflict the lungs of a subject. They can
 CC e.g. Ischemic conditions, pulmonary vasoconstrict
 CC asthma, impaired respiratory respiratory distress
 CC fibrosis, pulmonary hypertension, emphysema, lung
 CC pulmonary disease (COPD), and cancers such as lung
 CC carcinomas, and cancers which may metastasize to t
 CC breast and prostate cancer. The reduction of the
 CC the CNS reduces side effects. The A ventilation an
 CC release of deoxyadenosine which activates adenosin
 CC bronchoconstriction and inflammation. AAA34857 to
 CC nucleotide sequences given in the sequence listin
 CC invention, which correspond to SEQ ID NO:1 to 271
 CC 185 sequences are also called SEQ ID NO:1 to 185
 CC differ from the previously known sequences. SEQ ID
 CC (AAA3243 to AAA3392) are specifically claimed in
 CC invention. N.B. Sequences given in the disclosure
 CC invention do not match of each other correspondin
 CC given in the sequence list.
 XX Sequence 816 BP; 277 A; 147 G; 164 G; 218 T; 0 other;
 SU Query Match 67.1%; Score 231.4; H: 21;
 Best local Similarity 80.4%; Pred. No. 2,796-59;
 Matches 271; Conserved: 0; Mismatch: 66; Indels: 0; Gaps: 0;
 1 ATTTCGAGTGTGCACTGATGTTTATATACACCAAGAAATCTGCAGCTATAGCA 60
 446 ATTTCGATATATACCACTGATGTTTATATACACCAAGAAATCTGCAGCTATAGCA 387


```

1 COMPUTER READABLE FORM:
2 ZIP: 55402
3 MEDIUM TYPE: Diskette
4 OPERATING SYSTEM: DOS
5 SOFTWARE: FASTSEQ Version 2.0
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/89/155,984
8 FILING DATE: Unknown
9 CLASSIFICATION:
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: PCT/US97/059432
12 FILING DATE: 04-APR-1997
13 ATTORNEY/AGENT INFORMATION:
14 NAME: Viksnins, Ann S.
15 REGISTRATION NUMBER: 37,748
16 REFERENCE/WORKSHEET NUMBER: 150,167052
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: 612-359-3260
19 TELEFAX: 612-339-3061
20 TELEX:
21 INFORMATION FOR SEQ ID NO: 4:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 1534 base pairs
24 TYPE: nucleic acid
25 STRANDEDNESS: single
26 TOPOLOGY: linear
27 MOLECULE TYPE: cDNA
28 FEATURE:
29 NAME/KEY: mat.peptide
30 LOCATION: 104...442
31 OTHER INFORMATION:
32 US-09-155-884-4
33
34 Query Match 56.9%; Score 196.4; DB 4; Length 1534;
35 Best Local Similarity 73.4%; Pred No. 5,5e-53;
36 Matches 291; Gensequence 0; Mismatches 31; Indels 0; Gaps 0.
37
38 QY 2 CTTCGCGTGTGGACGTCCGCTGTATTATACGCCAAGAAATACITCAGAGIAATCIAGGAAC 61
39 | ||| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
40 Db 441 CCTTCGCGTGTGGACGTCCGCTGTATTATACGCCAAGAAATACITCAGAGIATCGAGAAC 380
41
42 QY 62 TTTCGCAGTGCACTTTTCTGCTGCAGACACTTTTTTTTACGCTGTATATGTGCTTTT 121
43 | || ||||| ||||| || ||||| || ||||| || ||||| || ||||| || |||||
44 Db 381 TGTCTGCTGCTGCTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 322
45
46 QY 122 ATTAACAACAATTTTGGAAATTTATACAAAGACCACCGGAGGAGAGAGAGAGAGAGAG 141
47 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
48 Db 321 ATTAAGAACAAGTTTGGAAATTTATACAAAGAGATTTGAGATTAAGAGAGAGAGAGAGAG 262
49
50 QY 192 AATGTGTGTATATGCTGAGAAAAGCTGCTTATATATAATTTATTTTATTTTATTTTAT 241
51 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
52 Db 261 AGATGTGTGTATATGCTGAGAAAAGCTGCTTATATATAATTTATTTTATTTTATTTTAT 202
53
54 QY 242 STAGCAATCATAGATTTTCAATCATATATATATATATATATATATATATATATATATATAT 201
55 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
56 Db 201 ATAGGAAGATCATATATATATATATATATATATATATATATATATATATATATATATAT 142
57
58 QY 302 AAGTGTGTGTATATGCTGAGAAAAGCTGCTTATATATAATTTATTTTATTTTATTTTAT 343
59 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
60 Db 141 AAGTGTGTGTATATGCTGAGAAAAGCTGCTTATATATAATTTATTTTATTTTATTTTAT 100
61
62 RESULT 5
63 US-08-629-643A-5/c
64 Sequence 5, Application US/0829643A
65 Patent No. 6025539
66 GENERAL INFORMATION:
67 APPLICANT: Lee, J. L.
68 APPLICANT: Lee, N. A.
69 TITLE OF INVENTION: IL-5 TRANSGENIC MOUSE
70 NUMBER OF SEQUENCES: 5
71 CORRESPONDENCE ADDRESS:

```

```

1 ADDRESS: Schomburg, Littlefield, Woessner & Kline
2 STREET: P.O. Box 7934
3 CITY: Minneapolis
4 STATE: MN
5 COUNTRY: USA
6 ZIP: 55402
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Diskette
10 COMPUTER: IBM Compatible
11 OPERATING SYSTEM: DOS
12 SOFTWARE: FASTSEQ Version 2.0
13 CURRENT APPLICATION NAME:
14 APPLICATION NUMBER: 007-00702-064VA
15 FILING DATE:
16 CLASSIFICATION: none
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: 007-00702-013
19 FILING DATE: 09-APR-1990
20 ATTORNEY/AGENT INFORMATION:
21 NAME: VIKSJOIN, Ann S
22 REGISTRATION NUMBER: 67,748
23 REFERENCE/CITEL NUMBER: 100-107001
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: 612-359-4264
26 TELEFAX: 612-359-4264
27 TELEX:
28 INFORMATION FOR SEQ ID NO: 1:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 6727 base pairs
31 TYPE: nucleic acid
32 STRANDNESS: single
33 TOPOLOGY: linear
34 MOLECULE TYPE: Genomic DNA
35 FEATURE:
36 NAME/KEY: mal-petide
37 LOCATION: 650...4771
38 OTHER INFORMATION: 007-00702-0730, 1560, 1572.
39 OTHER INFORMATION: 007-00702-0676, 0676...9771
40 US-HA-024-649A-5
41
42 Query Match 25% 3% Score 90.6, 18.0
43 Best local Similarity 70.6%, Prod. No. 4,5e+19
44 Matches 113 Conserved 100 Mismatches 44
45
46 Q1 83 CTCGACATTTTCTTCAGGGGCGGTATGCTTGCTTTGAAAG
47 TTTT TTTTTTTTTTTTTTTT TTTTTT TTTTTT TTTTTT
48 DB 3613 CTCGCCAGCATTTTCTTCAGGGGCGGTATGCTTTGAAAG
49 TTTT TTTTTTTTTTTTTTTT TTTTTT TTTTTT TTTTTT
50 Q2 143 AGATTATCCACTCAGGGGCGGTATGCTTTGAAAGT
51 TT TTTTTTTT TTTT TTTTTT TTTTTT TTTTTT
52 TT ATATTATCAATAATTTTCTTCAGGGGCGGTATGCTTTGAAAG
53 TTTT TTTTTTTTTTTTTTTT TTTTTT TTTTTT TTTTTT
54 Q3 203 ACTCTTATCATTAATTTGCTTTGAAAGT
55 TTTTTT TTTTTT TTTTTT TTTTTT TTTTTT
56 DB 3490 ATTCTGCATGCAATGCTTTGAAAGT
57 TTTT TTTTTTTTTTTTTTTT TTTTTT TTTTTT TTTTTT
58
59 RESULT 6
60 OS-05-280 733 1/c
61 Sequence 1, Application 08/020 790
62 Patent No. 6136603
63 GENERAL INFORMATION:
64 APPLICANT: Dean, Nicholas M.
65 APPLICANT: Karas, James G.
66 APPLICANT: McKay, Robert
67 TITLE OF INVENTION: ANTI-SERUM METABOLISM OF INDIKLE
68 FILE REFERENCE: TRANSITION
69 CURRENT APPLICATION NUMB ER: 007-00702-064VA
70 CURRENT FILING DATE: 1990 04 28
71 NUMBER OF SEQ ID NOS: 004
72 SOFTWARE: Patentin Vol. 2.0
73 SEQ ID NO 1

```

LENGTH: 6727
 TYPE: DNA
 ORGANISM: Mus musculus
 US-09-280-799-1

Query Match

Best Local Similarity 26.3% Score 90.6; DB 4; Length 6727;
 Host Local ID: 76.6% Prod. No. 4.4e-19;
 Matches 110; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

83 CCTGATACGTTTTTTTGGCGCTATGTGTCTTTATTAAGACAGTTTGGAA 142
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 140 CCTGATACGTTTATTTTGGCGCTATGTGTCTTTATTAAGACAGTTTGGAA 3551
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 143 AGTTAT 202
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 146 AGCATTTTCAT 3491
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 203 AGTTAT 227
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 146 AGTTAT 4456
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

RESULT 7

US-09-155-884-5/7

Sequence 5, Application US/0915584

Patent No. 6,215,040

GENERAL INFORMATION:

APPLICANT: James J. Lee et al.

TITLE OF INVENTION: IL-5 TRANSDUCTION RECEPTOR

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schwepman, Lundberg, Woessner & Kluh, P. A.

STREET: P. O. Box 2938

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE

OPERATING SYSTEM: DOS

SOFTWARE: FASTA version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/155,884

FILING DATE: UNKNOWN

CLASSIFICATION:

PRIOR APPLICATION DATA: PCT/US/97/07352

APPLICATION NUMBER: 09-APR-1997

AUTHOR/AGENT INFORMATION:

NAME: Viskochil, Ann S

REGISTRATION NUMBER: 37,748

REFERENCE/CHECK NUMBER: 150,167052

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-359-1360

TELEFAX: 612-349-3061

INDEX:

INFORMATION FOR SEQ. NO. 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 6727 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

FEATURE:

NAME/REV: 01/09/1997

LOCATION: 650,3771

OTHER INFORMATION: Join 658,770,1560,1592

OTHER INFORMATION: 3468,3590,3676,3771

US-09-155-884-5

Query Match 26.3% Score 90.6; DB 4; Length 6727;
 Best Local Similarity 76.6% Prod. No. 4.4e-19;
 Matches 110; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Matches 110; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

83 CCTGATACGTTTTTTTGGCGCTATGTGTCTTTATTAAGACAGTTTGGAA 142
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 140 CCTGATACGTTTATTTTGGCGCTATGTGTCTTTATTAAGACAGTTTGGAA 3551
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 143 AGTTAT 202
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 146 AGCATTTTCAT 3491
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 203 AGTTAT 227
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 146 AGTTAT 3466
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

RESULT 8

US-09-280-799-78/7

Sequence 79, Application US/09280799

Patent No. 6,156,608

GENERAL INFORMATION:

APPLICANT: Dean, Nicholas M

APPLICANT: Karris, James G

APPLICANT: McKay, Robert

TITLE OF INVENTION: ANTISENSE REGULATION OF INTERLEUKIN-5 SIGNAL

FILE REFERENCE: ISPH-0340

CURRENT APPLICATION NUMBER: US/09/280,799

CURRENT FILING DATE: 1999-04-26

NUMBER OF SEQ. NO. 208

SOFTWARE: Paton to Ver. 2.0

SEQ. ID NO 78

LENGTH: 4240

TYPE: DNA

ORGANISM: Homo sapiens

US-09-280-799-78

Query Match

Best Local Similarity 26.1% Score 90.2; DB 4; Length 4240;
 Host Local ID: 76.9% Prod. No. 4.4e-19;
 Matches 110; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

85 TGCACGCTTTTGTGCGCTATGTGTCTTTATTAAGACAGTTTGGAA 144
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 140 TGCACGCTTTTGTGCGCTATGTGTCTTTATTAAGACAGTTTGGAA 1964
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 145 TTATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 204
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 146 TCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1904
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 205 TCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 227
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 146 TCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1881
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

RESULT 9

US-09-280-799-78/7

Patent No. 6,156,608

APPLICANT: Dean, Nicholas M

APPLICANT: Karris, James G

APPLICANT: McKay, Robert

TITLE OF INVENTION: ANTISENSE REGULATION OF INTERLEUKIN-5 SIGNAL

FILE REFERENCE: ISPH-0340

CURRENT APPLICATION NUMBER: US/09/280,799

CURRENT FILING DATE: 1999-04-26

NUMBER OF SEQ. NO. 2

SOFTWARE: Paton to Ver. 2.0

SEQ. ID NO: 1

LENGTH: 4240

TYPE: DNA

ORGANISM: Homo sapiens

US-09-280-799-78

Query Match

Best Local Similarity 26.1% Score 90.2; DB 4; Length 4240;
 Host Local ID: 76.9% Prod. No. 4.4e-19;
 Matches 110; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

85 TGCACGCTTTTGTGCGCTATGTGTCTTTATTAAGACAGTTTGGAA 144
 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111

QY 238 AAGATAGATCATCAGTCCAGGCG 267
 Db 2124 TTGTGATTAATATTTTACATCGCC 2153

RESULT 15
 US-09-134-001C-150

Sequence 150, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NOCILEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

PRIOR FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 150

LENGTH: 927

TYPE: DNA

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-150

Query Match

Best Local Similarity 56.98; Pred. No. 1.1; Score 31.6; DB 4; Length 927;

Matches 58; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 199 AAAAATCTTTATGACAGTGTGATTTTATTTTCAGSAGTAGAATCATCAGGT 258

Db 523 ACAATAATCTTTATGACAAATTTAGTATTTATCTCAAAAGGCACTTTAAACGCAAT 582

QY 259 CGCATGCGCTATCAGCAATTTGATGAGTGGAGGACAGTGT 309

Db 583 ATAACGAAATAATGATTTATATGTTGGGGAAGCTGT 624

Search completed: November 7, 2002, 21:37:09
 Job time : 31.5622 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

4M nucleotide - nucleotide search, using sw model

Run on: November 7, 2002, 08:51:15 : Search time 6'09.366 seconds
(without alignments)
8739.041 Million-ops/second

File: US-09-755-633-11

Perfect score: 345

Sequence: 1 acattccggatgacacacacgg...atggagattctctacacacaa 345

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 889774376 residues

Total number of hits satisfying chosen Parameters: 22709122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Fast-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

EST:
1: em_estba:*
2: em_estbam:*
3: em_estcin:*
4: em_estcnu:*
5: em_estcnu:*
6: em_estcnu:*
7: em_estcnu:*
8: em_estcnu:*
9: em_estcnu:*
10: em_estcnu:*
11: em_estcnu:*
12: em_estcnu:*
13: em_estcnu:*
14: em_estcnu:*
15: em_estcnu:*
16: em_estcnu:*
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23: em_estcnu:*
24: em_estcnu:*
25: em_estcnu:*
26: em_estcnu:*
27: em_estcnu:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	78	22.6	14	B0596873 M1 P E4 a
2	40.6	11.8	522	B1676794 P1676794
3	39.8	11.5	535	A0376501 P1676794
4	49.2	11.4	608	B1328562 B1328562
5	39.2	11.4	619	B1328562 B1328562
6	39.2	11.4	905	A066243 P1676794

C 7	38.6	11.2	147	B143926
C 8	38	11.0	442	A060540
C 9	38	11.0	101	B0500181
C 10	37.8	11.0	104	B1526053
C 11	37.6	10.9	999	A2781738
C 12	37.4	10.8	965	C0802001
C 13	37.2	10.8	400	B1091941
C 14	37	10.7	601	B1140527
C 15	36.8	10.7	674	A0576964
C 16	36.8	10.7	674	A232668
C 17	36.8	10.7	914	B1682049
C 18	36.6	10.6	514	A0988461
C 19	36.4	10.6	567	A0679770
C 20	36.4	10.6	539	A0727133
C 21	36.4	10.6	589	A0796638
C 22	36.4	10.6	600	A0689939
C 23	36.4	10.6	609	A0572286
C 24	36.4	10.6	619	A0573786
C 25	36.4	10.6	632	A0952647
C 26	36.4	10.6	651	A0966596
C 27	36.4	10.6	652	A0926200
C 28	36.4	10.6	729	A042117
C 29	36.2	10.5	1342	C0804400
C 30	36	10.4	134	B0745748
C 31	36	10.4	590	A060223
C 32	36	10.4	626	B0194624
C 33	36	10.4	632	A079779
C 34	36	10.4	755	B1136376
C 35	35.8	10.4	499	A1001921
C 36	35.8	10.4	415	B0686534
C 37	35.8	10.4	766	A072806
C 38	35.8	10.4	1365	B1122703
C 39	35.6	10.3	275	B0409608
C 40	35.6	10.3	606	A0971495
C 41	35.6	10.3	607	A2460784
C 42	35.6	10.3	628	A0676350
C 43	35.6	10.3	844	C080303A
C 44	35.6	10.3	1075	C0804380
C 45	35.6	10.3	1101	C0801606

ALIGNMENTS

RESULT 1
B0596873
LOCUS
DEFINITION
M1 P E4 a
ACCESSION
B0596873
VERSION
B0596873.1
KEYWORDS
EST.
SOURCE
ORGANISM
Sus scrofa
Fukuyama; Molecular Biology of the Cell, 4th Edition, Vol. 1 (bases 1 to 500)
Normalisation and subtraction: two affine
discreetly
Genome Res. 6 (1996) 1006-1016
97044477
Contact: Toshiro CK
Molecular Genetics Laboratory, Department
Iowa State University
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Email: ckuang@iastate.edu
Tissue Procurement: by Chris Tushnet, Iowa
CDNA library preparation: by M. Porto St.
CDNA library: prepared by Dr. M. Porto St.
DNA Sequencing by: Dr. M. Porto St.

LOCUS	AA560540	432 bp	mRNA	linear	EST 18-AUG-1997
DEFINITION	W19405 rat Streptococcus mouse T-cell 93731 Mus musculus cDNA clone				

Accession
AF560540
replacing factor (MOUSE); mRNA sequence.
IMAGE:472705.57 similar to gb:X04601_cds2 Mouse mRNA for T-cell

```

VERSION      AA560540.1  GI:2332005
KEYWORDS     EST.

```

SOURCE:
ORGANISM

REFERENCE
1 (bases 1 to 432)
Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae, Murinae, Mus
Eukaryota; Metazoa; Chordata; Graminata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae, Murinae, Mus

AUTHORS
Marra, M., Hillier, L., Allen, M., Bowles, M., Pietrich, N., Putnam, T.
Ciselski, S., Kucada, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, N., Stepoe, M., Ian, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterson, R.

TITLE
The WashU-HHMI Mouse EST Project
Unpublished (1996)

